



1

SEQUENCE LISTING

<110> KIRCHHOFF, LOUIS V.
OTSU, KEIKO

<120> RECOMBINANT POLYPEPTIDES FOR DIAGNOSING INFECTION
WITH TRYPANOSOMA CRUZI

<130> 8372.003.US0000

<140> 10/726,692

<141> 2003-12-04

<150> 60/460,654

<151> 2002-12-04

<160> 57

<170> PatentIn Ver. 3.3

<210> 1

<211> 1521

<212> DNA

<213> Trypanosoma cruzi

<220>

<221> CDS

<222> (1)..(21)

<220>

<221> CDS

<222> (25)..(162)

<220>

<221> CDS

<222> (166)..(273)

<220>

<221> CDS

<222> (277)..(330)

<220>

<221> CDS

<222> (334)..(429)

<220>

<221> CDS

<222> (433)..(573)

<220>

<221> CDS

<222> (628)..(678)

<220>

<221> CDS

<222> (691)..(759)

<220>
<221> CDS
<222> (763) .. (834)

<220>
<221> CDS
<222> (838) .. (861)

<220>
<221> CDS
<222> (865) .. (876)

<220>
<221> CDS
<222> (880) .. (897)

<220>
<221> CDS
<222> (901) .. (918)

<220>
<221> CDS
<222> (922) .. (933)

<220>
<221> CDS
<222> (937) .. (948)

<220>
<221> CDS
<222> (952) .. (975)

<220>
<221> CDS
<222> (979) .. (1017)

<220>
<221> CDS
<222> (1021) .. (1059)

<220>
<221> CDS
<222> (1063) .. (1101)

<220>
<221> CDS
<222> (1105) .. (1143)

<220>
<221> CDS
<222> (1147) .. (1185)

<220>
<221> CDS
<222> (1189) .. (1227)

<220>
<221> CDS

<222> (1231)..(1269)

<220>

<221> CDS

<222> (1273)..(1311)

<220>

<221> CDS

<222> (1315)..(1353)

<220>

<221> CDS

<222> (1357)..(1395)

<220>

<221> CDS

<222> (1399)..(1437)

<220>

<221> CDS

<222> (1441)..(1479)

<220>

<221> CDS

<222> (1483)..(1521)

<220>

<221> CDS

<222> (577)..(624)

<220>

<221> CDS

<222> (682)..(687)

<400> 1

tat ggc ccg agc tgt ggt gct tga gga tgg agc gct tta cgt ggc gga	48
Tyr Gly Pro Ser Cys Gly Ala Gly Trp Ser Ala Leu Arg Gly Gly	
1 5 10 15	
caa tgc caa caa cct cgt tcg aga aat ctc caa tgg cgt tgt cac ttc	96
Gln Cys Gln Gln Pro Arg Ser Arg Asn Leu Gln Trp Arg Cys His Phe	
20 25 30	
gtt tat tac gga agg act gct ggg ccc atc gta cat caa acc gta cag	144
Val Tyr Tyr Gly Arg Thr Ala Gly Pro Ile Val His Gln Thr Val Gln	
35 40 45	
ccg tac aaa tgg cgc tca tga ctt gtt tgt gtc gga cac ggg caa atc	192
Pro Tyr Lys Trp Arg Ser Leu Val Cys Val Gly His Gly Gln Ile	
50 55 60	
acg cat cat ttt tgc ccc acc tca gaa aaa aac gtt cat cac agt gtt	240
Thr His His Phe Cys Pro Thr Ser Glu Lys Asn Val His His Ser Val	
65 70 75	
tat aac agg att cca gcc gga tgt tct tca aat tag cga gaa gag tcg	288
Tyr Asn Arg Ile Pro Ala Gly Cys Ser Ser Asn Arg Glu Glu Ser	
80 85 90	

ttt gat gtt tgc cat ctg caa ttc cac gaa aat tct tgc gat taa tat	336
Phe Asp Val Cys His Leu Gln Phe His Glu Asn Ser Cys Asp Tyr	
95 100 105	
gca ggg agc cac aac ccc gaa gga gta ctg gca agt tgg aaa tgc gga	384
Ala Gly Ser His Asn Pro Glu Gly Val Leu Ala Ser Trp Lys Cys Gly	
110 115 120	
ctg cat ggg cta tca gag ttc cct cat gct cac gac cga gga gga taa	432
Leu His Gly Leu Ser Glu Phe Pro His Ala His Asp Arg Gly Gly	
125 130 135	
act cct cta cta cgg cat att aaa tgg aac ccc atc cat cat gtc ttt	480
Thr Pro Leu Leu Arg His Ile Lys Trp Asn Pro Ile His His Val Phe	
140 145 150 155	
acc cgc cac caa aac gaa gac gga agc acc cag aat ttg ccc gga tgt	528
Thr Arg His Gln Asn Glu Asp Gly Ser Thr Gln Asn Leu Pro Gly Cys	
160 165 170	
gtt gtt gca gtg gcc aca tgg gcc cat tgt ttc gct tgt gaa tat taa	576
Val Val Ala Val Ala Thr Trp Ala His Cys Phe Ala Cys Glu Tyr	
175 180 185	
caa aca tgc att tta cgt tgt tac cgc ctc caa tgt ata cat tgt aca	624
Gln Thr Cys Ile Leu Arg Cys Tyr Arg Leu Gln Cys Ile His Cys Thr	
190 195 200	
tga tgg ctc gta tca tcc gac tgg atc cat ggc cca gct cca aca ggc	672
Trp Leu Val Ser Ser Asp Trp Ile His Gly Pro Ala Pro Thr Gly	
205 210 215	
aga aaa taa tat cac taa ttc caa aaa aga aat gac aaa gct acg aga	720
Arg Lys Tyr His Phe Gln Lys Arg Asn Asp Lys Ala Thr Arg	
220 225 230	
aaa agt gaa aaa ggc cga gaa aga aaa att gga cgc cat taa ccg ggc	768
Lys Ser Glu Lys Gly Arg Glu Arg Lys Ile Gly Arg His Pro Gly	
235 240 245	
aac caa gct gga aga gga acg aaa cca agc gta caa agc agc aca caa	816
Asn Gln Ala Gly Arg Gly Thr Lys Pro Ser Val Gln Ser Ser Thr Gln	
250 255 260	
ggc aga gga gga aaa ggc taa aac att tca acg cct tat aac att tga	864
Gly Arg Gly Gly Lys Gly Asn Ile Ser Thr Pro Tyr Asn Ile	
265 270 275	
gtc gga aaa tat taa ctt aaa gaa aag gcc aaa tga cgc agt ttc aaa	912
Val Gly Lys Tyr Leu Lys Glu Lys Ala Lys Arg Ser Phe Lys	
280 285 290	
tcg gga taa gaa aaa aaa ttc tga aac cgc aaa aac tga cga agt aga	960
Ser Gly Glu Lys Lys Phe Asn Arg Lys Asn Arg Ser Arg	
295 300	

gaa aca gag ggc ggc tga ggc tgc caa ggc cgt gga gac gga gaa gca	1008
Glu Thr Glu Gly Gly Gly Cys Gln Gly Arg Gly Asp Gly Glu Ala	
305 310 315	
gag ggc agc tga ggc cac gaa ggt tgc cga agc gga gaa gcg gaa ggc	1056
Glu Gly Ser Gly His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly	
320 325 330	
agc tga ggc cgc caa ggc cgt gga gac gga gaa gca gag ggc agc tga	1104
Ser Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser	
335 340 345	
agc cac gaa ggt tgc cga agc gga gaa gca gaa ggc agc tga ggc cgc	1152
Ser His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser Gly Arg	
350 355 360	
caa ggc cgt gga gac gga gaa gca gag ggc agc tga agc cac gaa ggt	1200
Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser Ser His Glu Gly	
365 370 375	
tgc cga agc gga gaa gca gag ggc agc tga agc cat gaa ggt tgc cga	1248
Cys Arg Ser Gly Glu Ala Glu Gly Ser Ser His Glu Gly Cys Arg	
380 385 390	
agc gga gaa gca gaa ggc agc tga ggc cgc caa ggc cgt gga gac gga	1296
Ser Gly Glu Ala Glu Gly Ser Gly Arg Gln Gly Arg Gly Asp Gly	
395 400 405	
gaa gca gag ggc agc tga agc cac gaa ggt tgc cga agc gga gaa gca	1344
Glu Ala Glu Gly Ser Ser His Glu Gly Cys Arg Ser Gly Glu Ala	
410 415 420	
gaa ggc agc tga ggc cgc caa ggc cgt gga gac gga gaa gca gag ggc	1392
Glu Gly Ser Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly	
425 430 435	
agc tga agc cac gaa ggt tgc cga agc gga gaa gca gaa ggc agc tga	1440
Ser Ser His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser	
440 445 450	
ggc cgc caa ggc cgt gga gac gga gaa gca gag ggc agc tga agc cac	1488
Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser Ser His	
455 460 465	
gaa ggt tgc cga agc gga gaa gga tat cga tcc	1521
Glu Gly Cys Arg Ser Gly Glu Gly Tyr Arg Ser	
470 475	

<210> 2

<211> 7

<212> PRT

<213> Trypanosoma cruzi

<400> 2

Tyr Gly Pro Ser Cys Gly Ala

1

5

<210> 3
 <211> 46
 <212> PRT
 <213> Trypanosoma cruzi

<400> 3
 Gly Trp Ser Ala Leu Arg Gly Gly Gln Cys Gln Gln Pro Arg Ser Arg
 1 5 10 15
 Asn Leu Gln Trp Arg Cys His Phe Val Tyr Tyr Gly Arg Thr Ala Gly
 20 25 30
 Pro Ile Val His Gln Thr Val Gln Pro Tyr Lys Trp Arg Ser
 35 40 45

<210> 4
 <211> 36
 <212> PRT
 <213> Trypanosoma cruzi

<400> 4
 Leu Val Cys Val Gly His Gly Gln Ile Thr His His Phe Cys Pro Thr
 1 5 10 15
 Ser Glu Lys Asn Val His His Ser Val Tyr Asn Arg Ile Pro Ala Gly
 20 25 30
 Cys Ser Ser Asn
 35

<210> 5
 <211> 18
 <212> PRT
 <213> Trypanosoma cruzi

<400> 5
 Arg Glu Glu Ser Phe Asp Val Cys His Leu Gln Phe His Glu Asn Ser
 1 5 10 15
 Cys Asp

<210> 6
 <211> 32
 <212> PRT
 <213> Trypanosoma cruzi

<400> 6
 Tyr Ala Gly Ser His Asn Pro Glu Gly Val Leu Ala Ser Trp Lys Cys
 1 5 10 15
 Gly Leu His Gly Leu Ser Glu Phe Pro His Ala His Asp Arg Gly Gly
 20 25 30

<210> 7
 <211> 47
 <212> PRT
 <213> Trypanosoma cruzi

<400> 7
 Thr Pro Leu Leu Arg His Ile Lys Trp Asn Pro Ile His His Val Phe
 1 5 10 15
 Thr Arg His Gln Asn Glu Asp Gly Ser Thr Gln Asn Leu Pro Gly Cys
 20 25 30
 Val Val Ala Val Ala Thr Trp Ala His Cys Phe Ala Cys Glu Tyr
 35 40 45

<210> 8
 <211> 16
 <212> PRT
 <213> Trypanosoma cruzi

<400> 8
 Gln Thr Cys Ile Leu Arg Cys Tyr Arg Leu Gln Cys Ile His Cys Thr
 1 5 10 15

<210> 9
 <211> 17
 <212> PRT
 <213> Trypanosoma cruzi

<400> 9
 Trp Leu Val Ser Ser Asp Trp Ile His Gly Pro Ala Pro Thr Gly Arg
 1 5 10 15
 Lys

<210> 10
 <211> 23
 <212> PRT
 <213> Trypanosoma cruzi

<400> 10
 Phe Gln Lys Arg Asn Asp Lys Ala Thr Arg Lys Ser Glu Lys Gly Arg
 1 5 10 15
 Glu Arg Lys Ile Gly Arg His
 20

<210> 11
 <211> 24
 <212> PRT
 <213> Trypanosoma cruzi

<400> 11
 Pro Gly Asn Gln Ala Gly Arg Gly Thr Lys Pro Ser Val Gln Ser Ser
 1 5 10 15

Thr Gln Gly Arg Gly Gly Lys Gly
20

<210> 12
<211> 8
<212> PRT
<213> Trypanosoma cruzi

<400> 12
Asn Ile Ser Thr Pro Tyr Asn Ile
1 5

<210> 13
<211> 4
<212> PRT
<213> Trypanosoma cruzi

<400> 13
Val Gly Lys Tyr
1

<210> 14
<211> 6
<212> PRT
<213> Trypanosoma cruzi

<400> 14
Leu Lys Glu Lys Ala Lys
1 5

<210> 15
<211> 6
<212> PRT
<213> Trypanosoma cruzi

<400> 15
Arg Ser Phe Lys Ser Gly
1 5

<210> 16
<211> 4
<212> PRT
<213> Trypanosoma cruzi

<400> 16
Glu Lys Lys Phe
1

<210> 17
<211> 4
<212> PRT
<213> Trypanosoma cruzi

<400> 17
Asn Arg Lys Asn
1

<210> 18
<211> 8
<212> PRT
<213> Trypanosoma cruzi

<400> 18
Arg Ser Arg Glu Thr Glu Gly Gly
1 5

<210> 19
<211> 13
<212> PRT
<213> Trypanosoma cruzi

<400> 19
Gly Cys Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser
1 5 10

<210> 20
<211> 13
<212> PRT
<213> Trypanosoma cruzi

<400> 20
Gly His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser
1 5 10

<210> 21
<211> 13
<212> PRT
<213> Trypanosoma cruzi

<400> 21
Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser
1 5 10

<210> 22
<211> 13
<212> PRT
<213> Trypanosoma cruzi

<400> 22
Ser His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser
1 5 10

<210> 23
<211> 13

<212> PRT

<213> Trypanosoma cruzi

<400> 23

Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser
1 5 10

<210> 24

<211> 13

<212> PRT

<213> Trypanosoma cruzi

<400> 24

Ser His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser
1 5 10

<210> 25

<211> 13

<212> PRT

<213> Trypanosoma cruzi

<400> 25

Ser His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser
1 5 10

<210> 26

<211> 13

<212> PRT

<213> Trypanosoma cruzi

<400> 26

Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser
1 5 10

<210> 27

<211> 13

<212> PRT

<213> Trypanosoma cruzi

<400> 27

Ser His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser
1 5 10

<210> 28

<211> 13

<212> PRT

<213> Trypanosoma cruzi

<400> 28

Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser
1 5 10

<210> 29
 <211> 13
 <212> PRT
 <213> Trypanosoma cruzi

<400> 29
 Ser His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser
 1 5 10

<210> 30
 <211> 13
 <212> PRT
 <213> Trypanosoma cruzi

<400> 30
 Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser
 1 5 10

<210> 31
 <211> 13
 <212> PRT
 <213> Trypanosoma cruzi

<400> 31
 Ser His Glu Gly Cys Arg Ser Gly Glu Gly Tyr Arg Ser
 1 5 10

<210> 32
 <211> 42
 <212> DNA
 <213> Trypanosoma cruzi

<220>
 <221> modified_base
 <222> (1)..(4)
 <223> a, t, c, g

<400> 32
 nnnnctatta ttgatacagt ttctgtacta tattggttgt gc

42

<210> 33
 <211> 3749
 <212> DNA
 <213> Trypanosoma cruzi

<220>
 <221> CDS
 <222> (833)..(2575)

<220>
 <221> sig_peptide
 <222> (822)..(937)

<220>

<221> mat_peptide

<222> (938)..(2575)

<400> 33

```

ccccctcgag gtcgacctgc aggtcaacgg atcttacctg agtacaaaag gtcaagtgag 60
cgggtcaaaag gatgtatata tacatatata accataaggg aaacatttgg gcattttaact 120
gcctttacat ttcccttttc cttcaatata ttgtttgttt gtttttggtt tctataggaa 180
attttaggat cgggccagcg gcataggaga ttattctctt ttttattaat tgcttaaatgc 240
gttggtctgt gtgtgtgttg gttcccttgt gcgagctcac ggggcctaata tatgattggt 300
gcgcatatgc atatatatat atatatatat acatgtgtgt gtgtgtgtat atgtacgttt 360
gttggtttgc cgctgtactc ccgcctgcgt gtgtctgtct ctctctctgt gtgtgtgatg 420
ggctgcttct ctttcttttg ttgcgtccct ttattattat tatttttttt tcttctctcc 480
cacttctctc ccctgttgtt gcacgcacag taaagataga gggagaaata gagcgagtgt 540
ttgtatcagt gtctccgttg cggctggtag tggtagaagg agaagaatag aagaaggaga 600
aaaaaaaaaa aaaaaaaaaa aaaagagaga gagagagaga agggcgaacg agaaaaaaga 660
agaagaaaca tttgagaagg aattggaacg aaaattgtaa gaggaagcaa aaaaaaaaaa 720
aaaaagtgtg tgtgtgtgag agagagagag agaggaagcc aataataata aaaagcaaac 780
aaaaaagcaa aaacaaaaat atttgtagac cggacgtccc gtcttggacg tg atg ttt 838
                                         Met Phe
                                         -35

tca aaa agg acg tcg cca gca ccc ttc cgt gcg ctc ctg ctg ccg gtc 886
Ser Lys Arg Thr Ser Pro Ala Pro Phe Arg Ala Leu Leu Leu Pro Val
          -30                -25                -20

gtg gtg gtg gtg gtg gtg gtg gca tct gtg gcc ctc cct gca gga 934
Val Val Val Val Val Val Val Val Val Ala Ser Val Ala Leu Pro Ala Gly
          -15                -10                -5

gcg cag ttt gat tta agg cag cag cag ctg gtt ata cag gat ttc ttc 982
Ala Gln Phe Asp Leu Arg Gln Gln Gln Leu Val Ile Gln Asp Phe Phe
   -1   1           5           10           15

atc agt cgc tcc tgc gca gga tgt tca cag ggg caa acc gat ggc cca 1030
Ile Ser Arg Ser Cys Ala Gly Cys Ser Gln Gly Gln Thr Asp Gly Pro
          20                25                30

agc ggt gcc ggc aca ctc ttc act gcc gcc ggt ggt tcg ctt ggc aaa 1078
Ser Gly Ala Gly Thr Leu Phe Thr Ala Ala Gly Gly Ser Leu Gly Lys
          35                40                45

gat gct tcc acg ctg ctg ttg tgt gac caa ggt ggt ggt ggc tcc agc 1126
Asp Ala Ser Thr Leu Leu Leu Cys Asp Gln Gly Gly Gly Gly Ser Ser
          50                55                60

```

gtg	cgt	ttg	gtg	aac	aaa	tcc	ggc	att	ttc	acc	ctt	gcc	ggt	agt	aaa	1174
Val	Arg	Leu	Val	Asn	Lys	Ser	Gly	Ile	Phe	Thr	Leu	Ala	Gly	Ser	Lys	
	65					70					75					
acg	acg	cgt	ggc	aat	caa	aat	ggt	ccg	gcg	gcg	acg	gca	ctc	ttc	aac	1222
Thr	Thr	Arg	Gly	Asn	Gln	Asn	Gly	Pro	Ala	Ala	Thr	Ala	Leu	Phe	Asn	
	80				85					90					95	
atg	ccc	cga	gct	gtg	gtg	ctt	gag	gat	gga	gcg	ctt	tac	gtg	gcg	gac	1270
Met	Pro	Arg	Ala	Val	Val	Leu	Glu	Asp	Gly	Ala	Leu	Tyr	Val	Ala	Asp	
				100					105					110		
agt	gcc	aac	aac	ctc	gtt	cga	gaa	atc	tcc	aat	ggc	att	gtc	act	tcg	1318
Ser	Ala	Asn	Asn	Leu	Val	Arg	Glu	Ile	Ser	Asn	Gly	Ile	Val	Thr	Ser	
			115					120					125			
ttt	att	acg	gag	gga	ctg	ctg	ggc	cca	tcg	tac	atc	aaa	ccg	tac	agc	1366
Phe	Ile	Thr	Glu	Gly	Leu	Leu	Gly	Pro	Ser	Tyr	Ile	Lys	Pro	Tyr	Ser	
		130					135					140				
cgt	cca	aat	ggc	gcc	cat	gac	ttg	ttt	gtg	tcg	gac	acg	ggc	aaa	tct	1414
Arg	Pro	Asn	Gly	Ala	His	Asp	Leu	Phe	Val	Ser	Asp	Thr	Gly	Lys	Ser	
	145					150					155					
cgc	atc	att	ttt	gcc	cca	ctt	cag	aaa	caa	acg	ttc	atc	aca	gtg	ttt	1462
Arg	Ile	Ile	Phe	Ala	Pro	Leu	Gln	Lys	Gln	Thr	Phe	Ile	Thr	Val	Phe	
	160				165					170					175	
ata	aca	gga	ttc	cag	ccg	gat	gtt	ctt	caa	att	agc	gag	aag	agt	cgt	1510
Ile	Thr	Gly	Phe	Gln	Pro	Asp	Val	Leu	Gln	Ile	Ser	Glu	Lys	Ser	Arg	
				180					185					190		
ttg	atg	ttt	gcc	atc	tgc	aat	tcc	acg	aaa	att	ctt	tcg	att	aat	atg	1558
Leu	Met	Phe	Ala	Ile	Cys	Asn	Ser	Thr	Lys	Ile	Leu	Ser	Ile	Asn	Met	
			195				200						205			
cag	gga	gcc	aca	acc	ccg	aag	gat	tac	tgg	caa	gtt	gga	aat	gcg	gac	1606
Gln	Gly	Ala	Thr	Thr	Pro	Lys	Asp	Tyr	Trp	Gln	Val	Gly	Asn	Ala	Asp	
		210					215					220				
tgc	atg	ggc	tat	cag	agt	tct	ctc	atg	ctc	acg	acc	gag	gag	gat	aaa	1654
Cys	Met	Gly	Tyr	Gln	Ser	Ser	Leu	Met	Leu	Thr	Thr	Glu	Glu	Asp	Lys	
	225					230					235					
ctc	ctc	tac	tac	ggc	ata	tta	aat	gga	acc	cca	tcc	atc	atg	tct	tta	1702
Leu	Leu	Tyr	Tyr	Gly	Ile	Leu	Asn	Gly	Thr	Pro	Ser	Ile	Met	Ser	Leu	
	240				245					250					255	
ccc	gcc	acc	aaa	acg	aag	acg	gaa	gca	ccc	aga	att	tgc	ccg	gat	gtg	1750
Pro	Ala	Thr	Lys	Thr	Lys	Thr	Glu	Ala	Pro	Arg	Ile	Cys	Pro	Asp	Val	
				260					265					270		
ttg	ttg	cgg	tgg	cca	cat	ggg	ccc	att	gtt	tcg	ctt	gtg	aat	att	aac	1798
Leu	Leu	Arg	Trp	Pro	His	Gly	Pro	Ile	Val	Ser	Leu	Val	Asn	Ile	Asn	
			275					280					285			

aaa cat gca ttt tac gtt gtt acc gcc tcc aat gta tac att gta cat	1846
Lys His Ala Phe Tyr Val Val Thr Ala Ser Asn Val Tyr Ile Val His	
290 295 300	
gat ggc tct tat cat ccg act gtg acg ccg aca cct cct ctg aca ccg	1894
Asp Gly Ser Tyr His Pro Thr Val Thr Pro Thr Pro Pro Leu Thr Pro	
305 310 315	
acg cct aca cca gaa gtg aca ccc aca cct act gtg acc ccg acg cct	1942
Thr Pro Thr Pro Glu Val Thr Pro Thr Pro Thr Val Thr Pro Thr Pro	
320 325 330 335	
aca ccg gaa gtg aca ccg aca ccg cca gtg act ccg agc ccc acc atc	1990
Thr Pro Glu Val Thr Pro Thr Pro Pro Val Thr Pro Ser Pro Thr Ile	
340 345 350	
aca atc cac cgg ggt ttt gct gtg gca gcc ttt cct gcc caa agt ctt	2038
Thr Ile His Arg Gly Phe Ala Val Ala Ala Phe Pro Ala Gln Ser Leu	
355 360 365	
cca atc gaa gac ccg cgg ctt atg cat gaa ctg ctt tct tgg tta atg	2086
Pro Ile Glu Asp Pro Arg Leu Met His Glu Leu Leu Ser Trp Leu Met	
370 375 380	
aag gat gta ggg att gcg ttc gaa tcc acg gac ttt ttt gcc gta ttt	2134
Lys Asp Val Gly Ile Ala Phe Glu Ser Thr Asp Phe Phe Ala Val Phe	
385 390 395	
cct cca gat aga gag gtt ttg gtg ccc ggt tat gta aat gtc tcc acc	2182
Pro Pro Asp Arg Glu Val Leu Val Pro Gly Tyr Val Asn Val Ser Thr	
400 405 410 415	
tgg aat aac ttg acg gtg cta ttc aac ttt gac cgc acc att gtc atc	2230
Trp Asn Asn Leu Thr Val Leu Phe Asn Phe Asp Arg Thr Ile Val Ile	
420 425 430	
acg gaa tat ttc act cca gag ggc atg tct tca gag gag gga cag gcc	2278
Thr Glu Tyr Phe Thr Pro Glu Gly Met Ser Ser Glu Glu Gly Gln Ala	
435 440 445	
cga ctc ttc gct tcg ccg tgg tac tgg acg aga aat ttc ctt gat tca	2326
Arg Leu Phe Ala Ser Pro Trp Tyr Trp Thr Arg Asn Phe Leu Asp Ser	
450 455 460	
tta aag aaa aca gta gct tgg aag gac ttg gag gcg ttt tgc atg gtc	2374
Leu Lys Lys Thr Val Ala Trp Lys Asp Leu Glu Ala Phe Cys Met Val	
465 470 475	
aac tgt gtt gaa cac tgt gag aca atg aca ttc cat aag tca gaa tgt	2422
Asn Cys Val Glu His Cys Glu Thr Met Thr Phe His Lys Ser Glu Cys	
480 485 490 495	
gta ggc tac gtc ccg ccc cca gta tgc aac gac gtc tgt gtg ggg gcg	2470
Val Gly Tyr Val Arg Pro Pro Val Cys Asn Asp Val Cys Val Gly Ala	
500 505 510	

gta gtg tcc tcc gtg gtg ctt ggc gcc aca ggt atc gca ctc att gca 2518
 Val Val Ser Ser Val Val Leu Gly Ala Thr Gly Ile Ala Leu Ile Ala
 515 520 525

ctg atg gtt gga agt tcg gcg aac tta cgg agc gct gtg att ctt gtt 2566
 Leu Met Val Gly Ser Ser Ala Asn Leu Arg Ser Ala Val Ile Leu Val
 530 535 540

cca ccc atg tagatTTTTgt cccacactt tggagaaagg tgggaaatga 2615
 Pro Pro Met
 545

cttcagaaat tgaaattaga aggaaccaac aacacaagaa gcaagcgaag gtgaaaacaa 2675

cgggaagaag aagaagaaga aaaaaaaaaa aagaaaagaa aaaaatgggg ggctgagtgg 2735

ggaaaagaga aagaaaagaa gtgtgcgtgt aaccgtgtgt gtgtgtgccg gggaaaaaga 2795

agaaacacaa aagatTTTctt ttttgtTTTT tgtTTtaatg gtgcaaagag ggaaacaaga 2855

aagcgaaggg tgcattgtgtg tctgttagata tataaaaaata aacatatgcc cccgcatgta 2915

ttttaccgtt ggcagttccg tggcttcttt tttttttttt tttttgtatt tttgttattt 2975

tttctcttta tttcttcgtg tgtgtgtgta tgtattatta ttcttttttg ttttttgttt 3035

gtttgtttgt ttttacctac tcatctgcct tcattttttt ttttgtgtgt tttcactcag 3095

ccccctcttc tttctctctt cttcttctct cttcatgcgt gtatttccgc atggagtggg 3155

aaaggaacgg ctgggagcga ttgtgatggt gcttgtgttg gaggtgtggc tatgagagta 3215

gtggagatgc atgtatgtat gtatatatgt ggtttggtgt atatatttaa atattatatg 3275

ttgttgttgt tgctgtccga ctctcggggg acgtacaccg acctacttac ttacagagag 3335

agagagagag aggaagagaa tgagagaaaa ggggggctg tgggtgtgtt tgtattcatt 3395

gaagagcgca aaaataaata aaaataaaat aataaaatga gggagagaga agggaggagg 3455

aaacagcaga ggaatttgta tgccatcggt gtgactaatt tttcataagg actctgtgat 3515

ggccctgtta accacgtcca ctgcagtaga cgagtcaaaa ttgactgcga gtgttacgcc 3575

aactgtacgt ctgtctccct cgtgctgtac gtgtgcaagt aagtacgtgt gtgcaactgtg 3635

cgtgtgcgtg tgtgtgtgtg tcaagggcgc cttttacgtg tctgtgcgct tgagtgggga 3695

ggggagaaga ggaggagaga cgaagaaaga aagaaagaaa aaagcgggcg gcgc 3749

<210> 34

<211> 581

<212> PRT

<213> Trypanosoma cruzi

<400> 34

Met	Phe	Ser	Lys	Arg	Thr	Ser	Pro	Ala	Pro	Phe	Arg	Ala	Leu	Leu	Leu
-35					-30					-25					-20
Pro	Val	Val	Val	Val	Val	Val	Val	Val	Val	Ala	Ser	Val	Ala	Leu	Pro
				-15					-10						-5
Ala	Gly	Ala	Gln	Phe	Asp	Leu	Arg	Gln	Gln	Gln	Leu	Val	Ile	Gln	Asp
	-1		1				5					10			
Phe	Phe	Ile	Ser	Arg	Ser	Cys	Ala	Gly	Cys	Ser	Gln	Gly	Gln	Thr	Asp
15						20					25				
Gly	Pro	Ser	Gly	Ala	Gly	Thr	Leu	Phe	Thr	Ala	Ala	Gly	Gly	Ser	Leu
30					35					40					45
Gly	Lys	Asp	Ala	Ser	Thr	Leu	Leu	Leu	Cys	Asp	Gln	Gly	Gly	Gly	Gly
				50					55						60
Ser	Ser	Val	Arg	Leu	Val	Asn	Lys	Ser	Gly	Ile	Phe	Thr	Leu	Ala	Gly
			65					70					75		
Ser	Lys	Thr	Thr	Arg	Gly	Asn	Gln	Asn	Gly	Pro	Ala	Ala	Thr	Ala	Leu
		80					85					90			
Phe	Asn	Met	Pro	Arg	Ala	Val	Val	Leu	Glu	Asp	Gly	Ala	Leu	Tyr	Val
95						100					105				
Ala	Asp	Ser	Ala	Asn	Asn	Leu	Val	Arg	Glu	Ile	Ser	Asn	Gly	Ile	Val
110					115					120					125
Thr	Ser	Phe	Ile	Thr	Glu	Gly	Leu	Leu	Gly	Pro	Ser	Tyr	Ile	Lys	Pro
				130					135					140	
Tyr	Ser	Arg	Pro	Asn	Gly	Ala	His	Asp	Leu	Phe	Val	Ser	Asp	Thr	Gly
			145					150					155		
Lys	Ser	Arg	Ile	Ile	Phe	Ala	Pro	Leu	Gln	Lys	Gln	Thr	Phe	Ile	Thr
		160					165					170			
Val	Phe	Ile	Thr	Gly	Phe	Gln	Pro	Asp	Val	Leu	Gln	Ile	Ser	Glu	Lys
175						180					185				
Ser	Arg	Leu	Met	Phe	Ala	Ile	Cys	Asn	Ser	Thr	Lys	Ile	Leu	Ser	Ile
190					195					200					205
Asn	Met	Gln	Gly	Ala	Thr	Thr	Pro	Lys	Asp	Tyr	Trp	Gln	Val	Gly	Asn
				210					215					220	
Ala	Asp	Cys	Met	Gly	Tyr	Gln	Ser	Ser	Leu	Met	Leu	Thr	Thr	Glu	Glu
			225					230					235		
Asp	Lys	Leu	Leu	Tyr	Tyr	Gly	Ile	Leu	Asn	Gly	Thr	Pro	Ser	Ile	Met
		240				245						250			
Ser	Leu	Pro	Ala	Thr	Lys	Thr	Lys	Thr	Glu	Ala	Pro	Arg	Ile	Cys	Pro
255						260					265				

Asp	Val	Leu	Leu	Arg	Trp	Pro	His	Gly	Pro	Ile	Val	Ser	Leu	Val	Asn	270	275	280	285
Ile	Asn	Lys	His	Ala	Phe	Tyr	Val	Val	Thr	Ala	Ser	Asn	Val	Tyr	Ile	290	295	300	
Val	His	Asp	Gly	Ser	Tyr	His	Pro	Thr	Val	Thr	Pro	Thr	Pro	Pro	Leu	305	310	315	
Thr	Pro	Thr	Pro	Thr	Pro	Glu	Val	Thr	Pro	Thr	Pro	Thr	Val	Thr	Pro	320	325	330	
Thr	Pro	Thr	Pro	Glu	Val	Thr	Pro	Thr	Pro	Pro	Val	Thr	Pro	Ser	Pro	335	340	345	
Thr	Ile	Thr	Ile	His	Arg	Gly	Phe	Ala	Val	Ala	Ala	Phe	Pro	Ala	Gln	350	355	360	365
Ser	Leu	Pro	Ile	Glu	Asp	Pro	Arg	Leu	Met	His	Glu	Leu	Leu	Ser	Trp	370	375	380	
Leu	Met	Lys	Asp	Val	Gly	Ile	Ala	Phe	Glu	Ser	Thr	Asp	Phe	Phe	Ala	385	390	395	
Val	Phe	Pro	Pro	Asp	Arg	Glu	Val	Leu	Val	Pro	Gly	Tyr	Val	Asn	Val	400	405	410	
Ser	Thr	Trp	Asn	Asn	Leu	Thr	Val	Leu	Phe	Asn	Phe	Asp	Arg	Thr	Ile	415	420	425	
Val	Ile	Thr	Glu	Tyr	Phe	Thr	Pro	Glu	Gly	Met	Ser	Ser	Glu	Glu	Gly	430	435	440	445
Gln	Ala	Arg	Leu	Phe	Ala	Ser	Pro	Trp	Tyr	Trp	Thr	Arg	Asn	Phe	Leu	450	455	460	
Asp	Ser	Leu	Lys	Lys	Thr	Val	Ala	Trp	Lys	Asp	Leu	Glu	Ala	Phe	Cys	465	470	475	
Met	Val	Asn	Cys	Val	Glu	His	Cys	Glu	Thr	Met	Thr	Phe	His	Lys	Ser	480	485	490	
Glu	Cys	Val	Gly	Tyr	Val	Arg	Pro	Pro	Val	Cys	Asn	Asp	Val	Cys	Val	495	500	505	
Gly	Ala	Val	Val	Ser	Ser	Val	Val	Leu	Gly	Ala	Thr	Gly	Ile	Ala	Leu	510	515	520	525
Ile	Ala	Leu	Met	Val	Gly	Ser	Ser	Ala	Asn	Leu	Arg	Ser	Ala	Val	Ile	530	535	540	
Leu	Val	Pro	Pro	Met												545			

<210> 35

<211> 2151

<212> DNA

<213> Trypanosoma cruzi

<220>

<221> CDS

<222> (1)..(2151)

<400> 35

atg gcc cga gct gtg gtg ctt gag gat gga gcg ctt tac gtg gcg gac	48
Met Ala Arg Ala Val Val Leu Glu Asp Gly Ala Leu Tyr Val Ala Asp	
1 5 10 15	
aat gcc aac aac ctc gtt cga gaa atc tcc aat ggc gtt gtc act tcg	96
Asn Ala Asn Asn Leu Val Arg Glu Ile Ser Asn Gly Val Val Thr Ser	
20 25 30	
ttt att acg gaa gga ctg ctg ggc cca tcg tac atc aaa ccg tac agc	144
Phe Ile Thr Glu Gly Leu Leu Gly Pro Ser Tyr Ile Lys Pro Tyr Ser	
35 40 45	
cgt aca aat ggc gct cat gac ttg ttt gtg tcg gac acg ggc aaa tca	192
Arg Thr Asn Gly Ala His Asp Leu Phe Val Ser Asp Thr Gly Lys Ser	
50 55 60	
cgc atc att ttt gcc cca cct cag aaa aaa acg ttc atc aca gtg ttt	240
Arg Ile Ile Phe Ala Pro Pro Gln Lys Lys Thr Phe Ile Thr Val Phe	
65 70 75 80	
ata aca gga ttc cag ccg gat gtt ctt caa att agc gag aag agt cgt	288
Ile Thr Gly Phe Gln Pro Asp Val Leu Gln Ile Ser Glu Lys Ser Arg	
85 90 95	
ttg atg ttt gcc atc tgc aat tcc acg aaa att ctt gcg att aat atg	336
Leu Met Phe Ala Ile Cys Asn Ser Thr Lys Ile Leu Ala Ile Asn Met	
100 105 110	
cag gga gcc aca acc ccg aag gag tac tgg caa gtt gga aat gcg gac	384
Gln Gly Ala Thr Thr Pro Lys Glu Tyr Trp Gln Val Gly Asn Ala Asp	
115 120 125	
tgc atg ggc tat cag agt tcc ctc atg ctc acg acc gag gag gat aaa	432
Cys Met Gly Tyr Gln Ser Ser Leu Met Leu Thr Thr Glu Glu Asp Lys	
130 135 140	
ctc ctc tac tac ggc ata tta aat gga acc cca tcc atc atg tct tta	480
Leu Leu Tyr Tyr Gly Ile Leu Asn Gly Thr Pro Ser Ile Met Ser Leu	
145 150 155 160	
ccc gcc acc aaa acg aag acg gaa gca ccc aga att tgc ccg gat gtg	528
Pro Ala Thr Lys Thr Lys Thr Glu Ala Pro Arg Ile Cys Pro Asp Val	
165 170 175	
ttg ttg cag tgg cca cat ggg ccc att gtt tcg ctt gtg aat att aac	576
Leu Leu Gln Trp Pro His Gly Pro Ile Val Ser Leu Val Asn Ile Asn	
180 185 190	
aaa cat gca ttt tac gtt gtt acc gcc tcc aat gta tac att gta cat	624
Lys His Ala Phe Tyr Val Val Thr Ala Ser Asn Val Tyr Ile Val His	
195 200 205	

gat ggc tcg tat cat ccg act gga tcc atg gcc cag ctc caa cag gca	672
Asp Gly Ser Tyr His Pro Thr Gly Ser Met Ala Gln Leu Gln Gln Ala	
210 215 220	
 gaa aat aat atc act aat tcc aaa aaa gaa atg aca aag cta cga gaa	720
Glu Asn Asn Ile Thr Asn Ser Lys Lys Glu Met Thr Lys Leu Arg Glu	
225 230 235 240	
 aaa gtg aaa aag gcc gag aaa gaa aaa ttg gac gcc att aac cgg gca	768
Lys Val Lys Lys Ala Glu Lys Glu Lys Leu Asp Ala Ile Asn Arg Ala	
245 250 255	
 acc aag ctg gaa gag gaa cga aac caa gcg tac aaa gca gca cac aag	816
Thr Lys Leu Glu Glu Glu Arg Asn Gln Ala Tyr Lys Ala Ala His Lys	
260 265 270	
 gca gag gag gaa aag gct aaa aca ttt caa cgc ctt ata aca ttt gag	864
Ala Glu Glu Glu Lys Ala Lys Thr Phe Gln Arg Leu Ile Thr Phe Glu	
275 280 285	
 tcg gaa aat att aac tta aag aaa agg cca aat gac gca gtt tca aat	912
Ser Glu Asn Ile Asn Leu Lys Lys Arg Pro Asn Asp Ala Val Ser Asn	
290 295 300	
 cgg gat aag aaa aaa aat tct gaa acc gca aaa act gac gaa gta gag	960
Arg Asp Lys Lys Lys Asn Ser Glu Thr Ala Lys Thr Asp Glu Val Glu	
305 310 315 320	
 aaa cag agg gcg gct gag gct gcc aag gcc gtg gag acg gag aag cag	1008
Lys Gln Arg Ala Ala Glu Ala Ala Lys Ala Val Glu Thr Glu Lys Gln	
325 330 335	
 agg gca gct gag gcc acg aag gtt gcc gaa gcg gag aag cgg aag gca	1056
Arg Ala Ala Glu Ala Thr Lys Val Ala Glu Ala Glu Lys Arg Lys Ala	
340 345 350	
 gct gag gcc gcc aag gcc gtg gag acg gag aag cag agg gca gct gaa	1104
Ala Glu Ala Ala Lys Ala Val Glu Thr Glu Lys Gln Arg Ala Ala Glu	
355 360 365	
 gcc acg aag gtt gcc gaa gcg gag aag cag aag gca gct gag gcc gcc	1152
Ala Thr Lys Val Ala Glu Ala Glu Lys Gln Lys Ala Ala Glu Ala Ala	
370 375 380	
 aag gcc gtg gag acg gag aag cag agg gca gct gaa gcc acg aag gtt	1200
Lys Ala Val Glu Thr Glu Lys Gln Arg Ala Ala Glu Ala Thr Lys Val	
385 390 395 400	
 gcc gaa gcg gag aag cag agg gca gct gaa gcc atg aag gtt gcc gaa	1248
Ala Glu Ala Glu Lys Gln Arg Ala Ala Glu Ala Met Lys Val Ala Glu	
405 410 415	
 gcg gag aag cag aag gca gct gag gcc gcc aag gcc gtg gag acg gag	1296
Ala Glu Lys Gln Lys Ala Ala Glu Ala Ala Lys Ala Val Glu Thr Glu	
420 425 430	

aag	cag	agg	gca	gct	gaa	gcc	acg	aag	gtt	gcc	gaa	gcg	gag	aag	cag	1344
Lys	Gln	Arg	Ala	Ala	Glu	Ala	Thr	Lys	Val	Ala	Glu	Ala	Glu	Lys	Gln	
		435					440					445				
aag	gca	gct	gag	gcc	gcc	aag	gcc	gtg	gag	acg	gag	aag	cag	agg	gca	1392
Lys	Ala	Ala	Glu	Ala	Ala	Lys	Ala	Val	Glu	Thr	Glu	Lys	Gln	Arg	Ala	
	450					455					460					
gct	gaa	gcc	acg	aag	gtt	gcc	gaa	gcg	gag	aag	cag	aag	gca	gct	gag	1440
Ala	Glu	Ala	Thr	Lys	Val	Ala	Glu	Ala	Glu	Lys	Gln	Lys	Ala	Ala	Glu	
465					470					475					480	
gcc	gcc	aag	gcc	gtg	gag	acg	gag	aag	cag	agg	gca	gct	gaa	gcc	acg	1488
Ala	Ala	Lys	Ala	Val	Glu	Thr	Glu	Lys	Gln	Arg	Ala	Ala	Glu	Ala	Thr	
			485				490						495			
aag	gtt	gcc	gaa	gcg	gag	aag	gat	atc	gat	ccc	atg	ggg	gct	tgt	ggg	1536
Lys	Val	Ala	Glu	Ala	Glu	Lys	Asp	Ile	Asp	Pro	Met	Gly	Ala	Cys	Gly	
		500					505					510				
tcg	aag	gac	tcg	acg	agc	gac	aag	ggg	ttg	gcg	agc	gat	aag	gac	ggc	1584
Ser	Lys	Asp	Ser	Thr	Ser	Asp	Lys	Gly	Leu	Ala	Ser	Asp	Lys	Asp	Gly	
		515					520					525				
aag	aac	gcc	aag	gac	cgc	aag	gaa	gcg	tgg	gag	cgc	att	cgc	cag	gcg	1632
Lys	Asn	Ala	Lys	Asp	Arg	Lys	Glu	Ala	Trp	Glu	Arg	Ile	Arg	Gln	Ala	
	530					535					540					
att	cct	cgt	gag	aag	acc	gcc	gag	gca	aaa	cag	cgc	cgc	atc	gag	ctc	1680
Ile	Pro	Arg	Glu	Lys	Thr	Ala	Glu	Ala	Lys	Gln	Arg	Arg	Ile	Glu	Leu	
545					550					555					560	
ttc	aag	aag	ttc	gac	aag	aac	gag	acc	ggg	aag	ctg	tgc	tac	gat	gag	1728
Phe	Lys	Lys	Phe	Asp	Lys	Asn	Glu	Thr	Gly	Lys	Leu	Cys	Tyr	Asp	Glu	
			565						570					575		
gtg	cac	agc	ggc	tgc	ctc	gag	gtg	ctg	aag	ttg	gac	gag	ttc	acg	ccg	1776
Val	His	Ser	Gly	Cys	Leu	Glu	Val	Leu	Lys	Leu	Asp	Glu	Phe	Thr	Pro	
			580					585					590			
cga	gtg	cgc	gac	atc	acg	aag	cgt	gca	ttc	gac	aag	gcg	agg	gcc	ctg	1824
Arg	Val	Arg	Asp	Ile	Thr	Lys	Arg	Ala	Phe	Asp	Lys	Ala	Arg	Ala	Leu	
		595					600					605				
ggc	agc	aag	ctg	gag	aac	aag	ggc	tcc	gag	gac	ttt	gtt	gaa	ttt	ctg	1872
Gly	Ser	Lys	Leu	Glu	Asn	Lys	Gly	Ser	Glu	Asp	Phe	Val	Glu	Phe	Leu	
	610					615					620					
gag	ttc	cgt	ctg	atg	ctg	tgc	tac	atc	tac	gac	ttc	ttc	gag	ctg	acg	1920
Glu	Phe	Arg	Leu	Met	Leu	Cys	Tyr	Ile	Tyr	Asp	Phe	Phe	Glu	Leu	Thr	
625					630					635					640	
gtg	atg	ttc	gac	gag	att	gac	gcc	tcc	ggc	aac	atg	ctg	gtt	gac	gag	1968
Val	Met	Phe	Asp	Glu	Ile	Asp	Ala	Ser	Gly	Asn	Met	Leu	Val	Asp	Glu	
				645					650					655		

gag gag ttc aag cgc gcc gtg ccc aag ctt gag gcg tgg ggc gcc aag 2016
 Glu Glu Phe Lys Arg Ala Val Pro Lys Leu Glu Ala Trp Gly Ala Lys
 660 665 670

gtc gag gat ccc gcg gcg ctg ttc aag gag ctc gat aag aac ggc act 2064
 Val Glu Asp Pro Ala Ala Leu Phe Lys Glu Leu Asp Lys Asn Gly Thr
 675 680 685

ggg tcc gtg acg ttc gac gag ttt gct gcg tgg gct tct gca gtc aaa 2112
 Gly Ser Val Thr Phe Asp Glu Phe Ala Ala Trp Ala Ser Ala Val Lys
 690 695 700

ctg gac gcc gac ggc gac ccg gac aac gtg ccg gat atc 2151
 Leu Asp Ala Asp Gly Asp Pro Asp Asn Val Pro Asp Ile
 705 710 715

<210> 36

<211> 717

<212> PRT

<213> Trypanosoma cruzi

<400> 36

Met Ala Arg Ala Val Val Leu Glu Asp Gly Ala Leu Tyr Val Ala Asp
 1 5 10 15

Asn Ala Asn Asn Leu Val Arg Glu Ile Ser Asn Gly Val Val Thr Ser
 20 25 30

Phe Ile Thr Glu Gly Leu Leu Gly Pro Ser Tyr Ile Lys Pro Tyr Ser
 35 40 45

Arg Thr Asn Gly Ala His Asp Leu Phe Val Ser Asp Thr Gly Lys Ser
 50 55 60

Arg Ile Ile Phe Ala Pro Pro Gln Lys Lys Thr Phe Ile Thr Val Phe
 65 70 75 80

Ile Thr Gly Phe Gln Pro Asp Val Leu Gln Ile Ser Glu Lys Ser Arg
 85 90 95

Leu Met Phe Ala Ile Cys Asn Ser Thr Lys Ile Leu Ala Ile Asn Met
 100 105 110

Gln Gly Ala Thr Thr Pro Lys Glu Tyr Trp Gln Val Gly Asn Ala Asp
 115 120 125

Cys Met Gly Tyr Gln Ser Ser Leu Met Leu Thr Thr Glu Glu Asp Lys
 130 135 140

Leu Leu Tyr Tyr Gly Ile Leu Asn Gly Thr Pro Ser Ile Met Ser Leu
 145 150 155 160

Pro Ala Thr Lys Thr Lys Thr Glu Ala Pro Arg Ile Cys Pro Asp Val
 165 170 175

Leu Leu Gln Trp Pro His Gly Pro Ile Val Ser Leu Val Asn Ile Asn
 180 185 190

Lys	His	Ala	Phe	Tyr	Val	Val	Thr	Ala	Ser	Asn	Val	Tyr	Ile	Val	His
	195						200					205			
Asp	Gly	Ser	Tyr	His	Pro	Thr	Gly	Ser	Met	Ala	Gln	Leu	Gln	Gln	Ala
	210					215					220				
Glu	Asn	Asn	Ile	Thr	Asn	Ser	Lys	Lys	Glu	Met	Thr	Lys	Leu	Arg	Glu
225					230					235					240
Lys	Val	Lys	Lys	Ala	Glu	Lys	Glu	Lys	Leu	Asp	Ala	Ile	Asn	Arg	Ala
				245					250					255	
Thr	Lys	Leu	Glu	Glu	Glu	Arg	Asn	Gln	Ala	Tyr	Lys	Ala	Ala	His	Lys
		260						265					270		
Ala	Glu	Glu	Glu	Lys	Ala	Lys	Thr	Phe	Gln	Arg	Leu	Ile	Thr	Phe	Glu
		275					280					285			
Ser	Glu	Asn	Ile	Asn	Leu	Lys	Lys	Arg	Pro	Asn	Asp	Ala	Val	Ser	Asn
	290					295					300				
Arg	Asp	Lys	Lys	Lys	Asn	Ser	Glu	Thr	Ala	Lys	Thr	Asp	Glu	Val	Glu
305					310					315					320
Lys	Gln	Arg	Ala	Ala	Glu	Ala	Ala	Lys	Ala	Val	Glu	Thr	Glu	Lys	Gln
			325						330					335	
Arg	Ala	Ala	Glu	Ala	Thr	Lys	Val	Ala	Glu	Ala	Glu	Lys	Arg	Lys	Ala
		340						345					350		
Ala	Glu	Ala	Ala	Lys	Ala	Val	Glu	Thr	Glu	Lys	Gln	Arg	Ala	Ala	Glu
		355					360					365			
Ala	Thr	Lys	Val	Ala	Glu	Ala	Glu	Lys	Gln	Lys	Ala	Ala	Glu	Ala	Ala
	370					375					380				
Lys	Ala	Val	Glu	Thr	Glu	Lys	Gln	Arg	Ala	Ala	Glu	Ala	Thr	Lys	Val
385					390					395					400
Ala	Glu	Ala	Glu	Lys	Gln	Arg	Ala	Ala	Glu	Ala	Met	Lys	Val	Ala	Glu
			405						410					415	
Ala	Glu	Lys	Gln	Lys	Ala	Ala	Glu	Ala	Ala	Lys	Ala	Val	Glu	Thr	Glu
		420					425						430		
Lys	Gln	Arg	Ala	Ala	Glu	Ala	Thr	Lys	Val	Ala	Glu	Ala	Glu	Lys	Gln
		435					440					445			
Lys	Ala	Ala	Glu	Ala	Ala	Lys	Ala	Val	Glu	Thr	Glu	Lys	Gln	Arg	Ala
	450					455					460				
Ala	Glu	Ala	Thr	Lys	Val	Ala	Glu	Ala	Glu	Lys	Gln	Lys	Ala	Ala	Glu
465					470				475						480
Ala	Ala	Lys	Ala	Val	Glu	Thr	Glu	Lys	Gln	Arg	Ala	Ala	Glu	Ala	Thr
			485					490					495		

Lys Val Ala Glu Ala Glu Lys Asp Ile Asp Pro Met Gly Ala Cys Gly
 500 505 510
 Ser Lys Asp Ser Thr Ser Asp Lys Gly Leu Ala Ser Asp Lys Asp Gly
 515 520 525
 Lys Asn Ala Lys Asp Arg Lys Glu Ala Trp Glu Arg Ile Arg Gln Ala
 530 535 540
 Ile Pro Arg Glu Lys Thr Ala Glu Ala Lys Gln Arg Arg Ile Glu Leu
 545 550 555 560
 Phe Lys Lys Phe Asp Lys Asn Glu Thr Gly Lys Leu Cys Tyr Asp Glu
 565 570 575
 Val His Ser Gly Cys Leu Glu Val Leu Lys Leu Asp Glu Phe Thr Pro
 580 585 590
 Arg Val Arg Asp Ile Thr Lys Arg Ala Phe Asp Lys Ala Arg Ala Leu
 595 600 605
 Gly Ser Lys Leu Glu Asn Lys Gly Ser Glu Asp Phe Val Glu Phe Leu
 610 615 620
 Glu Phe Arg Leu Met Leu Cys Tyr Ile Tyr Asp Phe Phe Glu Leu Thr
 625 630 635 640
 Val Met Phe Asp Glu Ile Asp Ala Ser Gly Asn Met Leu Val Asp Glu
 645 650 655
 Glu Glu Phe Lys Arg Ala Val Pro Lys Leu Glu Ala Trp Gly Ala Lys
 660 665 670
 Val Glu Asp Pro Ala Ala Leu Phe Lys Glu Leu Asp Lys Asn Gly Thr
 675 680 685
 Gly Ser Val Thr Phe Asp Glu Phe Ala Ala Trp Ala Ser Ala Val Lys
 690 695 700
 Leu Asp Ala Asp Gly Asp Pro Asp Asn Val Pro Asp Ile
 705 710 715

<210> 37
 <211> 1836
 <212> DNA
 <213> Trypanosoma cruzi

<220>
 <221> CDS
 <222> (1)..(1836)

<400> 37
 atg gag cag gag cgc agg cag ctg ctc gag aag gac ccg cgc agg aac 48
 Met Glu Gln Glu Arg Arg Gln Leu Leu Glu Lys Asp Pro Arg Arg Asn
 1 5 10 15

gcg aag gag atc gct gcg ctt gag gag agc atg aat gcc cgc gca cag	96
Ala Lys Glu Ile Ala Ala Leu Glu Glu Ser Met Asn Ala Arg Ala Gln	
20 25 30	
gag ctg gca cgc gag aag aag ctt gct gac cgc gcg ttc ctc gac cag	144
Glu Leu Ala Arg Glu Lys Lys Leu Ala Asp Arg Ala Phe Leu Asp Gln	
35 40 45	
aag ccg gag ggc gtg ccg ctg cga gag ctg ccg ctc gac gac gac agc	192
Lys Pro Glu Gly Val Pro Leu Arg Glu Leu Pro Leu Asp Asp Asp Ser	
50 55 60	
gac ttt gtt gct atg gag cag gag cgc agg cag ctg ctc gag aag gac	240
Asp Phe Val Ala Met Glu Gln Glu Arg Arg Gln Leu Leu Glu Lys Asp	
65 70 75 80	
ccg cgc agg aac gcg aag gag atc gct gcg ctt gag gag agc atg aat	288
Pro Arg Arg Asn Ala Lys Glu Ile Ala Ala Leu Glu Glu Ser Met Asn	
85 90 95	
gcc cgc gca cag gag ctg gca cgc gag aag aag ctt gct gac cgc gcg	336
Ala Arg Ala Gln Glu Leu Ala Arg Glu Lys Lys Leu Ala Asp Arg Ala	
100 105 110	
ttc ctc gac cag aag ccg gag ggc gtg ccg ctg cga gag ctg ccg ctc	384
Phe Leu Asp Gln Lys Pro Glu Gly Val Pro Leu Arg Glu Leu Pro Leu	
115 120 125	
gac gac gac agc gac ttt gtt gct atg gag cag gag cgc agg cag ctg	432
Asp Asp Asp Ser Asp Phe Val Ala Met Glu Gln Glu Arg Arg Gln Leu	
130 135 140	
ctc gag aag gac ccg cgc agg aac gcg aag gag atc gct gcg ctt gag	480
Leu Glu Lys Asp Pro Arg Arg Asn Ala Lys Glu Ile Ala Ala Leu Glu	
145 150 155 160	
gag agc atg aat gcc cgc gca cag gag ctg gca cgc gag aag aag ctt	528
Glu Ser Met Asn Ala Arg Ala Gln Glu Leu Ala Arg Glu Lys Lys Leu	
165 170 175	
gct gac cgc gcg ttc ctc gac cag aag ccg gag ggc gtg ccg ctg cga	576
Ala Asp Arg Ala Phe Leu Asp Gln Lys Pro Glu Gly Val Pro Leu Arg	
180 185 190	
gag ctg ccg ctc gac gac gac agc gac ttt gtt gct atg gag cag gag	624
Glu Leu Pro Leu Asp Asp Asp Ser Asp Phe Val Ala Met Glu Gln Glu	
195 200 205	
cgc agg cag ctg ctc gag aag gac ccg cgc agg aac gcg aag gag atc	672
Arg Arg Gln Leu Leu Glu Lys Asp Pro Arg Arg Asn Ala Lys Glu Ile	
210 215 220	
gct gcg ctt gag gag agc atg aat gcc cgc gca cag gag ctg gca cgc	720
Ala Ala Leu Glu Glu Ser Met Asn Ala Arg Ala Gln Glu Leu Ala Arg	
225 230 235 240	

gag	aag	aag	ctt	gct	gac	cgc	gcg	ttc	ctc	gac	cag	aag	ccg	gag	ggc	768
Glu	Lys	Lys	Leu	Ala	Asp	Arg	Ala	Phe	Leu	Asp	Gln	Lys	Pro	Glu	Gly	
			245					250						255		
gtg	ccg	ctg	cga	gag	ctg	ccg	ctc	gac	gac	gac	agc	gac	ttt	gtt	gct	816
Val	Pro	Leu	Arg	Glu	Leu	Pro	Leu	Asp	Asp	Asp	Ser	Asp	Phe	Val	Ala	
			260					265					270			
atg	gag	cag	gag	cgc	agg	cag	ctg	ctc	gag	aag	gac	ccg	cgc	agg	aac	864
Met	Glu	Gln	Glu	Arg	Arg	Gln	Leu	Leu	Glu	Lys	Asp	Pro	Arg	Arg	Asn	
		275					280					285				
gcg	aag	gag	atc	gct	gcg	ctt	gag	gag	agc	atg	aat	gcc	cgc	gca	cag	912
Ala	Lys	Glu	Ile	Ala	Ala	Leu	Glu	Glu	Ser	Met	Asn	Ala	Arg	Ala	Gln	
	290					295					300					
gag	ctg	gca	cgc	gag	aag	aag	ctt	gct	gac	cgc	gcg	ttc	ctc	gac	cag	960
Glu	Leu	Ala	Arg	Glu	Lys	Lys	Leu	Ala	Asp	Arg	Ala	Phe	Leu	Asp	Gln	
305					310				315					320		
aag	ccg	gag	ggc	gtg	ccg	ctg	cga	gag	ctg	ccg	ctc	gac	gac	gac	agc	1008
Lys	Pro	Glu	Gly	Val	Pro	Leu	Arg	Glu	Leu	Pro	Leu	Asp	Asp	Asp	Ser	
			325					330					335			
gac	ttt	gtt	gct	atg	gag	cag	gag	cgc	agg	cag	ctg	ctc	gag	aag	gac	1056
Asp	Phe	Val	Ala	Met	Glu	Gln	Glu	Arg	Arg	Gln	Leu	Leu	Glu	Lys	Asp	
			340					345					350			
ccg	cgc	agg	aac	gcg	aag	gag	atc	gct	gcg	ctt	gag	gag	agc	atg	aat	1104
Pro	Arg	Arg	Asn	Ala	Lys	Glu	Ile	Ala	Ala	Leu	Glu	Glu	Ser	Met	Asn	
		355					360					365				
gcc	cgc	gca	cag	gag	ctg	gca	cgc	gag	aag	aag	ctt	gct	gac	cgc	gcg	1152
Ala	Arg	Ala	Gln	Glu	Leu	Ala	Arg	Glu	Lys	Lys	Leu	Ala	Asp	Arg	Ala	
	370					375					380					
ttc	ctc	gac	cag	aag	ccg	gag	ggc	gtg	ccg	ctg	cga	gag	ctg	ccg	ctc	1200
Phe	Leu	Asp	Gln	Lys	Pro	Glu	Gly	Val	Pro	Leu	Arg	Glu	Leu	Pro	Leu	
385					390				395					400		
gac	gac	gac	agc	gac	ttt	gtt	gct	atg	gag	cag	gag	cgc	agg	cag	ctg	1248
Asp	Asp	Asp	Ser	Asp	Phe	Val	Ala	Met	Glu	Gln	Glu	Arg	Arg	Gln	Leu	
			405					410					415			
ctc	gag	aag	gac	ccg	cgc	agg	aac	gcg	aag	gag	atc	gct	gcg	ctt	gag	1296
Leu	Glu	Lys	Asp	Pro	Arg	Arg	Asn	Ala	Lys	Glu	Ile	Ala	Ala	Leu	Glu	
			420					425				430				
gag	agc	atg	aat	gcc	cgc	gca	cag	gag	ctg	gca	cgc	gag	aag	aag	ctt	1344
Glu	Ser	Met	Asn	Ala	Arg	Ala	Gln	Glu	Leu	Ala	Arg	Glu	Lys	Lys	Leu	
		435					440					445				
gct	gac	cgc	gcg	ttc	ctc	gac	cag	aag	ccg	gag	ggc	gtg	ccg	ctg	cga	1392
Ala	Asp	Arg	Ala	Phe	Leu	Asp	Gln	Lys	Pro	Glu	Gly	Val	Pro	Leu	Arg	
	450					455					460					

gag ctg ccg ctc gac gac gac agc gac ttt gtt gct atg gag cag gag 1440
 Glu Leu Pro Leu Asp Asp Asp Ser Asp Phe Val Ala Met Glu Gln Glu
 465 470 475 480

cgc agg cag ctg ctc gag aag gac ccg cgc agg aac gcg aag gag atc 1488
 Arg Arg Gln Leu Leu Glu Lys Asp Pro Arg Arg Asn Ala Lys Glu Ile
 485 490 495

gct gcg ctt gag gag agc atg aat gcc cgc gca cag gag ctg gca cgc 1536
 Ala Ala Leu Glu Glu Ser Met Asn Ala Arg Ala Gln Glu Leu Ala Arg
 500 505 510

gag aag aag ctt gct gac cgc gcg ttc ctc gac cag aag ccg gag ggc 1584
 Glu Lys Lys Leu Ala Asp Arg Ala Phe Leu Asp Gln Lys Pro Glu Gly
 515 520 525

gtg ccg ctg cga gag ctg ccg ctc gac gac gac agc gac ttt gtt gct 1632
 Val Pro Leu Arg Glu Leu Pro Leu Asp Asp Asp Ser Asp Phe Val Ala
 530 535 540

atg gag cag gag cgc agg cag ctg ctc gag aag gac ccg cgc agg aac 1680
 Met Glu Gln Glu Arg Arg Gln Leu Leu Glu Lys Asp Pro Arg Arg Asn
 545 550 555 560

gcg aag gag atc gct gcg ctt gag gag agc atg aat gcc cgc gca cag 1728
 Ala Lys Glu Ile Ala Ala Leu Glu Glu Ser Met Asn Ala Arg Ala Gln
 565 570 575

gag ctg gca cgc gag aag aag ctt gct gac cgc gcg ttc ctc gac cag 1776
 Glu Leu Ala Arg Glu Lys Lys Leu Ala Asp Arg Ala Phe Leu Asp Gln
 580 585 590

aag ccg gag ggc gtg ccg ctg cga gag ctg ccg ctc gac gac gac agc 1824
 Lys Pro Glu Gly Val Pro Leu Arg Glu Leu Pro Leu Asp Asp Asp Ser
 595 600 605

gac ttt gtt gct 1836
 Asp Phe Val Ala
 610

<210> 38

<211> 612

<212> PRT

<213> Trypanosoma cruzi

<400> 38

Met Glu Gln Glu Arg Arg Gln Leu Leu Glu Lys Asp Pro Arg Arg Asn
 1 5 10 15

Ala Lys Glu Ile Ala Ala Leu Glu Glu Ser Met Asn Ala Arg Ala Gln
 20 25 30

Glu Leu Ala Arg Glu Lys Lys Leu Ala Asp Arg Ala Phe Leu Asp Gln
 35 40 45

Lys Pro Glu Gly Val Pro Leu Arg Glu Leu Pro Leu Asp Asp Asp Ser
 50 55 60

Asp	Phe	Val	Ala	Met	Glu	Gln	Glu	Arg	Arg	Gln	Leu	Leu	Glu	Lys	Asp	65	70	75	80
Pro	Arg	Arg	Asn	Ala	Lys	Glu	Ile	Ala	Ala	Leu	Glu	Glu	Ser	Met	Asn	85	90	95	
Ala	Arg	Ala	Gln	Glu	Leu	Ala	Arg	Glu	Lys	Lys	Leu	Ala	Asp	Arg	Ala	100	105	110	
Phe	Leu	Asp	Gln	Lys	Pro	Glu	Gly	Val	Pro	Leu	Arg	Glu	Leu	Pro	Leu	115	120	125	
Asp	Asp	Asp	Ser	Asp	Phe	Val	Ala	Met	Glu	Gln	Glu	Arg	Arg	Gln	Leu	130	135	140	
Leu	Glu	Lys	Asp	Pro	Arg	Arg	Asn	Ala	Lys	Glu	Ile	Ala	Ala	Leu	Glu	145	150	155	160
Glu	Ser	Met	Asn	Ala	Arg	Ala	Gln	Glu	Leu	Ala	Arg	Glu	Lys	Lys	Leu	165	170	175	
Ala	Asp	Arg	Ala	Phe	Leu	Asp	Gln	Lys	Pro	Glu	Gly	Val	Pro	Leu	Arg	180	185	190	
Glu	Leu	Pro	Leu	Asp	Asp	Asp	Ser	Asp	Phe	Val	Ala	Met	Glu	Gln	Glu	195	200	205	
Arg	Arg	Gln	Leu	Leu	Glu	Lys	Asp	Pro	Arg	Arg	Asn	Ala	Lys	Glu	Ile	210	215	220	
Ala	Ala	Leu	Glu	Glu	Ser	Met	Asn	Ala	Arg	Ala	Gln	Glu	Leu	Ala	Arg	225	230	235	240
Glu	Lys	Lys	Leu	Ala	Asp	Arg	Ala	Phe	Leu	Asp	Gln	Lys	Pro	Glu	Gly	245	250	255	
Val	Pro	Leu	Arg	Glu	Leu	Pro	Leu	Asp	Asp	Asp	Ser	Asp	Phe	Val	Ala	260	265	270	
Met	Glu	Gln	Glu	Arg	Arg	Gln	Leu	Leu	Glu	Lys	Asp	Pro	Arg	Arg	Asn	275	280	285	
Ala	Lys	Glu	Ile	Ala	Ala	Leu	Glu	Glu	Ser	Met	Asn	Ala	Arg	Ala	Gln	290	295	300	
Glu	Leu	Ala	Arg	Glu	Lys	Lys	Leu	Ala	Asp	Arg	Ala	Phe	Leu	Asp	Gln	305	310	315	320
Lys	Pro	Glu	Gly	Val	Pro	Leu	Arg	Glu	Leu	Pro	Leu	Asp	Asp	Asp	Ser	325	330	335	
Asp	Phe	Val	Ala	Met	Glu	Gln	Glu	Arg	Arg	Gln	Leu	Leu	Glu	Lys	Asp	340	345	350	
Pro	Arg	Arg	Asn	Ala	Lys	Glu	Ile	Ala	Ala	Leu	Glu	Glu	Ser	Met	Asn	355	360	365	

Ala Arg Ala Gln Glu Leu Ala Arg Glu Lys Lys Leu Ala Asp Arg Ala
 370 375 380
 Phe Leu Asp Gln Lys Pro Glu Gly Val Pro Leu Arg Glu Leu Pro Leu
 385 390 395 400
 Asp Asp Asp Ser Asp Phe Val Ala Met Glu Gln Glu Arg Arg Gln Leu
 405 410 415
 Leu Glu Lys Asp Pro Arg Arg Asn Ala Lys Glu Ile Ala Ala Leu Glu
 420 425 430
 Glu Ser Met Asn Ala Arg Ala Gln Glu Leu Ala Arg Glu Lys Lys Leu
 435 440 445
 Ala Asp Arg Ala Phe Leu Asp Gln Lys Pro Glu Gly Val Pro Leu Arg
 450 455 460
 Glu Leu Pro Leu Asp Asp Asp Ser Asp Phe Val Ala Met Glu Gln Glu
 465 470 475 480
 Arg Arg Gln Leu Leu Glu Lys Asp Pro Arg Arg Asn Ala Lys Glu Ile
 485 490 495
 Ala Ala Leu Glu Glu Ser Met Asn Ala Arg Ala Gln Glu Leu Ala Arg
 500 505 510
 Glu Lys Lys Leu Ala Asp Arg Ala Phe Leu Asp Gln Lys Pro Glu Gly
 515 520 525
 Val Pro Leu Arg Glu Leu Pro Leu Asp Asp Asp Ser Asp Phe Val Ala
 530 535 540
 Met Glu Gln Glu Arg Arg Gln Leu Leu Glu Lys Asp Pro Arg Arg Asn
 545 550 555 560
 Ala Lys Glu Ile Ala Ala Leu Glu Glu Ser Met Asn Ala Arg Ala Gln
 565 570 575
 Glu Leu Ala Arg Glu Lys Lys Leu Ala Asp Arg Ala Phe Leu Asp Gln
 580 585 590
 Lys Pro Glu Gly Val Pro Leu Arg Glu Leu Pro Leu Asp Asp Asp Ser
 595 600 605
 Asp Phe Val Ala
 610

<210> 39
 <211> 621
 <212> DNA
 <213> Trypanosoma cruzi

<220>
 <221> CDS
 <222> (1)..(621)

<400> 39

ttt	aat	cct	tct	acg	gac	aaa	ttg	aag	cta	aac	caa	caa	aat	aag	cct	48
Phe	Asn	Pro	Ser	Thr	Asp	Lys	Leu	Lys	Leu	Asn	Gln	Gln	Asn	Lys	Pro	
1				5					10					15		
cat	att	gca	aat	aat	aaa	caa	aaa	aca	aca	ctc	gaa	aaa	act	caa	aca	96
His	Ile	Ala	Asn	Asn	Lys	Gln	Lys	Thr	Thr	Leu	Glu	Lys	Thr	Gln	Thr	
			20					25					30			
gaa	caa	aaa	aca	gcg	cca	ttt	gga	cag	ggc	gca	gca	ggg	tgg	aca	aaa	144
Glu	Gln	Lys	Thr	Ala	Pro	Phe	Gly	Gln	Gly	Ala	Ala	Gly	Trp	Thr	Lys	
		35					40					45				
cca	tca	cca	ttt	gga	cag	gcc	gca	gca	ggg	gac	aaa	cca	cca	cca	ttt	192
Pro	Ser	Pro	Phe	Gly	Gln	Ala	Ala	Ala	Gly	Asp	Lys	Pro	Pro	Pro	Phe	
	50					55					60					
gga	cag	gcc	gca	gca	ggg	gac	aaa	cca	cca	cca	ttt	gga	cag	gcc	gca	240
Gly	Gln	Ala	Ala	Ala	Gly	Asp	Lys	Pro	Pro	Pro	Phe	Gly	Gln	Ala	Ala	
65					70					75					80	
gca	ggg	gac	aaa	cca	tca	cta	ttt	gga	cag	gcc	gca	gca	ggg	gac	aaa	288
Ala	Gly	Asp	Lys	Pro	Ser	Leu	Phe	Gly	Gln	Ala	Ala	Ala	Gly	Asp	Lys	
				85				90						95		
cca	tca	cca	ttt	gga	cag	gcc	gca	gca	ggg	gac	aaa	cca	cca	cca	ttt	336
Pro	Ser	Pro	Phe	Gly	Gln	Ala	Ala	Ala	Gly	Asp	Lys	Pro	Pro	Pro	Phe	
			100					105					110			
gga	cag	gcc	gca	gca	ggg	gac	aaa	cca	tca	cta	ttt	gga	cag	gcc	gca	384
Gly	Gln	Ala	Ala	Ala	Gly	Asp	Lys	Pro	Ser	Leu	Phe	Gly	Gln	Ala	Ala	
		115					120					125				
gca	ggg	gac	aaa	cca	tca	cca	ttt	gga	cag	gcc	gca	gca	ggg	gac	aaa	432
Ala	Gly	Asp	Lys	Pro	Ser	Pro	Phe	Gly	Gln	Ala	Ala	Ala	Gly	Asp	Lys	
	130					135				140						
cca	cca	cca	ttt	gga	cag	gcc	gca	gca	ggg	gac	aaa	cca	cca	cca	ttt	480
Pro	Pro	Pro	Phe	Gly	Gln	Ala	Ala	Ala	Gly	Asp	Lys	Pro	Pro	Pro	Phe	
145					150					155					160	
gga	cag	gcc	gca	gca	ggg	gac	aaa	cca	tca	cta	ttt	gga	cag	gcc	gca	528
Gly	Gln	Ala	Ala	Ala	Gly	Asp	Lys	Pro	Ser	Leu	Phe	Gly	Gln	Ala	Ala	
			165					170					175			
gca	ggg	gac	aaa	cca	tca	cca	ttt	gga	cag	gga	act	gcg	ttt	gat	gcc	576
Ala	Gly	Asp	Lys	Pro	Ser	Pro	Phe	Gly	Gln	Gly	Thr	Ala	Phe	Asp	Ala	
			180					185					190			
tct	cga	agc	act	gtg	ttt	gcg	aat	gcg	cct	ggg	gtt	gcc	cag	gtg		621
Ser	Arg	Ser	Thr	Val	Phe	Ala	Asn	Ala	Pro	Gly	Val	Ala	Gln	Val		
		195					200					205				

<210> 40

<211> 207

<212> PRT

<213> Trypanosoma cruzi

<400> 40

```

Phe Asn Pro Ser Thr Asp Lys Leu Lys Leu Asn Gln Gln Asn Lys Pro
 1          5          10          15

His Ile Ala Asn Asn Lys Gln Lys Thr Thr Leu Glu Lys Thr Gln Thr
      20          25          30

Glu Gln Lys Thr Ala Pro Phe Gly Gln Gly Ala Ala Gly Trp Thr Lys
      35          40          45

Pro Ser Pro Phe Gly Gln Ala Ala Ala Gly Asp Lys Pro Pro Pro Phe
      50          55          60

Gly Gln Ala Ala Ala Gly Asp Lys Pro Pro Pro Phe Gly Gln Ala Ala
      65          70          75          80

Ala Gly Asp Lys Pro Ser Leu Phe Gly Gln Ala Ala Ala Gly Asp Lys
      85          90          95

Pro Ser Pro Phe Gly Gln Ala Ala Ala Gly Asp Lys Pro Pro Pro Phe
      100          105          110

Gly Gln Ala Ala Ala Gly Asp Lys Pro Ser Leu Phe Gly Gln Ala Ala
      115          120          125

Ala Gly Asp Lys Pro Ser Pro Phe Gly Gln Ala Ala Ala Gly Asp Lys
      130          135          140

Pro Pro Pro Phe Gly Gln Ala Ala Ala Gly Asp Lys Pro Pro Pro Phe
      145          150          155          160

Gly Gln Ala Ala Ala Gly Asp Lys Pro Ser Leu Phe Gly Gln Ala Ala
      165          170          175

Ala Gly Asp Lys Pro Ser Pro Phe Gly Gln Gly Thr Ala Phe Asp Ala
      180          185          190

Ser Arg Ser Thr Val Phe Ala Asn Ala Pro Gly Val Ala Gln Val
      195          200          205

```

<210> 41

<211> 1845

<212> DNA

<213> Trypanosoma cruzi

<220>

<221> CDS

<222> (1)..(1845)

<400> 41

```

ttt aat cct tct acg gac aaa ttg aag cta aac caa caa aat aag cct   48
Phe Asn Pro Ser Thr Asp Lys Leu Lys Leu Asn Gln Gln Asn Lys Pro
 1          5          10          15

```

cat att gca aat aat aaa caa aaa aca aca ctc gaa aaa act caa aca	96
His Ile Ala Asn Asn Lys Gln Lys Thr Thr Leu Glu Lys Thr Gln Thr	
20 25 30	
gaa caa aaa aca gcg cca ttt gga cag ggc gca gca ggg tgg aca aaa	144
Glu Gln Lys Thr Ala Pro Phe Gly Gln Gly Ala Ala Gly Trp Thr Lys	
35 40 45	
cca tca cca ttt gga cag gcc gca gca ggt gac aaa cca cca cca ttt	192
Pro Ser Pro Phe Gly Gln Ala Ala Ala Gly Asp Lys Pro Pro Pro Phe	
50 55 60	
gga cag gcc gca gca ggt gac aaa cca cca cca ttt gga cag gcc gca	240
Gly Gln Ala Ala Ala Gly Asp Lys Pro Pro Pro Phe Gly Gln Ala Ala	
65 70 75 80	
gca ggt gac aaa cca tca cta ttt gga cag gcc gca gca ggt gac aaa	288
Ala Gly Asp Lys Pro Ser Leu Phe Gly Gln Ala Ala Ala Gly Asp Lys	
85 90 95	
cca tca cca ttt gga cag gcc gca gca ggt gac aaa cca cca cca ttt	336
Pro Ser Pro Phe Gly Gln Ala Ala Ala Gly Asp Lys Pro Pro Pro Phe	
100 105 110	
gga cag gcc gca gca ggt gac aaa cca tca cta ttt gga cag gcc gca	384
Gly Gln Ala Ala Ala Gly Asp Lys Pro Ser Leu Phe Gly Gln Ala Ala	
115 120 125	
gca ggt gac aaa cca tca cca ttt gga cag gcc gca gca ggt gac aaa	432
Ala Gly Asp Lys Pro Ser Pro Phe Gly Gln Ala Ala Ala Gly Asp Lys	
130 135 140	
cca cca cca ttt gga cag gcc gca gca ggt gac aaa cca cca cca ttt	480
Pro Pro Pro Phe Gly Gln Ala Ala Ala Gly Asp Lys Pro Pro Pro Phe	
145 150 155 160	
gga cag gcc gca gca ggt gac aaa cca tca cta ttt gga cag gcc gca	528
Gly Gln Ala Ala Ala Gly Asp Lys Pro Ser Leu Phe Gly Gln Ala Ala	
165 170 175	
gca ggt gac aaa cca tca cca ttt gga cag gga act gcg ttt gat gcc	576
Ala Gly Asp Lys Pro Ser Pro Phe Gly Gln Gly Thr Ala Phe Asp Ala	
180 185 190	
tct cga agc act gtg ttt gcg aat gcg cct ggt gtt gcc cag gtg atg	624
Ser Arg Ser Thr Val Phe Ala Asn Ala Pro Gly Val Ala Gln Val Met	
195 200 205	
gag cag gag cgc agg cag ctg ctc gag aag gac ccg cgc agg aac gcg	672
Glu Gln Glu Arg Arg Gln Leu Leu Glu Lys Asp Pro Arg Arg Asn Ala	
210 215 220	
aag gag atc gct gcg ctt gag gag agc atg aat gcc cgc gca cag gag	720
Lys Glu Ile Ala Ala Leu Glu Glu Ser Met Asn Ala Arg Ala Gln Glu	
225 230 235 240	

ctg gca cgc gag aag aag ctt gct gac cgc gcg ttc ctc gac cag aag	768
Leu Ala Arg Glu Lys Lys Leu Ala Asp Arg Ala Phe Leu Asp Gln Lys	
245 250 255	
ccg gag ggc gtg ccg ctg cga gag ctg ccg ctc gac gac gac agc gac	816
Pro Glu Gly Val Pro Leu Arg Glu Leu Pro Leu Asp Asp Asp Ser Asp	
260 265 270	
ttt gtt gct atg gag cag gag cgc agg cag ctg ctc gag aag gac ccg	864
Phe Val Ala Met Glu Gln Glu Arg Arg Gln Leu Leu Glu Lys Asp Pro	
275 280 285	
cgc agg aac gcg aag gag atc gct gcg ctt gag gag agc atg aat gcc	912
Arg Arg Asn Ala Lys Glu Ile Ala Ala Leu Glu Glu Ser Met Asn Ala	
290 295 300	
cgc gca cag gag ctg gca cgc gag aag aag ctt gct gac cgc gcg ttc	960
Arg Ala Gln Glu Leu Ala Arg Glu Lys Lys Leu Ala Asp Arg Ala Phe	
305 310 315 320	
ctc gac cag aag ccg gag ggc gtg ccg ctg cga gag ctg ccg ctc gac	1008
Leu Asp Gln Lys Pro Glu Gly Val Pro Leu Arg Glu Leu Pro Leu Asp	
325 330 335	
gac gac agc gac ttt gtt gct atg gag cag gag cgc agg cag ctg ctc	1056
Asp Asp Ser Asp Phe Val Ala Met Glu Gln Glu Arg Arg Gln Leu Leu	
340 345 350	
gag aag gac ccg cgc agg aac gcg aag gag atc gct gcg ctt gag gag	1104
Glu Lys Asp Pro Arg Arg Asn Ala Lys Glu Ile Ala Ala Leu Glu Glu	
355 360 365	
agc atg aat gcc cgc gca cag gag ctg gca cgc gag aag aag ctt gct	1152
Ser Met Asn Ala Arg Ala Gln Glu Leu Ala Arg Glu Lys Lys Leu Ala	
370 375 380	
gac cgc gcg ttc ctc gac cag aag ccg gag ggc gtg ccg ctg cga gag	1200
Asp Arg Ala Phe Leu Asp Gln Lys Pro Glu Gly Val Pro Leu Arg Glu	
385 390 395 400	
ctg ccg ctc gac gac gac agc gac ttt gtt gct atg gag cag gag cgc	1248
Leu Pro Leu Asp Asp Asp Ser Asp Phe Val Ala Met Glu Gln Glu Arg	
405 410 415	
agg cag ctg ctc gag aag gac ccg cgc agg aac gcg aag gag atc gct	1296
Arg Gln Leu Leu Glu Lys Asp Pro Arg Arg Asn Ala Lys Glu Ile Ala	
420 425 430	
gcg ctt gag gag agc atg aat gcc cgc gca cag gag ctg gca cgc gag	1344
Ala Leu Glu Glu Ser Met Asn Ala Arg Ala Gln Glu Leu Ala Arg Glu	
435 440 445	
aag aag ctt gct gac cgc gcg ttc ctc gac cag aag ccg gag ggc gtg	1392
Lys Lys Leu Ala Asp Arg Ala Phe Leu Asp Gln Lys Pro Glu Gly Val	
450 455 460	

ccg	ctg	cga	gag	ctg	ccg	ctc	gac	gac	gac	agc	gac	ttt	gtt	gct	atg	1440
Pro	Leu	Arg	Glu	Leu	Pro	Leu	Asp	Asp	Asp	Ser	Asp	Phe	Val	Ala	Met	
465					470					475					480	
gag	cag	gag	cgc	agg	cag	ctg	ctc	gag	aag	gac	ccg	cgc	agg	aac	gcg	1488
Glu	Gln	Glu	Arg	Arg	Gln	Leu	Leu	Glu	Lys	Asp	Pro	Arg	Arg	Asn	Ala	
			485						490					495		
aag	gag	atc	gct	gcg	ctt	gag	gag	agc	atg	aat	gcc	cgc	gca	cag	gag	1536
Lys	Glu	Ile	Ala	Ala	Leu	Glu	Glu	Ser	Met	Asn	Ala	Arg	Ala	Gln	Glu	
			500					505					510			
ctg	gca	cgc	gag	aag	aag	ctt	gct	gac	cgc	gcg	ttc	ctc	gac	cag	aag	1584
Leu	Ala	Arg	Glu	Lys	Lys	Leu	Ala	Asp	Arg	Ala	Phe	Leu	Asp	Gln	Lys	
		515					520					525				
ccg	gag	ggc	gtg	ccg	ctg	cga	gag	ctg	ccg	ctc	gac	gac	gac	agc	gac	1632
Pro	Glu	Gly	Val	Pro	Leu	Arg	Glu	Leu	Pro	Leu	Asp	Asp	Asp	Ser	Asp	
	530					535					540					
ttt	gtt	gct	atg	gag	cag	gag	cgc	agg	cag	ctg	ctc	gag	aag	gac	ccg	1680
Phe	Val	Ala	Met	Glu	Gln	Glu	Arg	Arg	Gln	Leu	Leu	Glu	Lys	Asp	Pro	
545					550				555						560	
cgc	agg	aac	gcg	aag	gag	atc	gct	gcg	ctt	gag	gag	agc	atg	aat	gcc	1728
Arg	Arg	Asn	Ala	Lys	Glu	Ile	Ala	Ala	Leu	Glu	Glu	Ser	Met	Asn	Ala	
				565					570					575		
cgc	gca	cag	gag	ctg	gca	cgc	gag	aag	aag	ctt	gct	gac	cgc	gcg	ttc	1776
Arg	Ala	Gln	Glu	Leu	Ala	Arg	Glu	Lys	Lys	Leu	Ala	Asp	Arg	Ala	Phe	
			580					585					590			
ctc	gac	cag	aag	ccg	gag	ggc	gtg	ccg	ctg	cga	gag	ctg	ccg	ctc	gac	1824
Leu	Asp	Gln	Lys	Pro	Glu	Gly	Val	Pro	Leu	Arg	Glu	Leu	Pro	Leu	Asp	
		595					600					605				
gac	gac	agc	gac	ttt	gtt	gct										1845
Asp	Asp	Ser	Asp	Phe	Val	Ala										
	610					615										

<210> 42

<211> 615

<212> PRT

<213> Trypanosoma cruzi

<400> 42

Phe	Asn	Pro	Ser	Thr	Asp	Lys	Leu	Lys	Leu	Asn	Gln	Gln	Asn	Lys	Pro
1				5					10					15	

His	Ile	Ala	Asn	Asn	Lys	Gln	Lys	Thr	Thr	Leu	Glu	Lys	Thr	Gln	Thr
		20					25						30		

Glu	Gln	Lys	Thr	Ala	Pro	Phe	Gly	Gln	Gly	Ala	Ala	Gly	Trp	Thr	Lys
		35					40					45			

Pro	Ser	Pro	Phe	Gly	Gln	Ala	Ala	Ala	Gly	Asp	Lys	Pro	Pro	Pro	Phe
	50					55					60				

Gly	Gln	Ala	Ala	Ala	Gly	Asp	Lys	Pro	Pro	Pro	Phe	Gly	Gln	Ala	Ala		
65					70					75						80	
Ala	Gly	Asp	Lys	Pro	Ser	Leu	Phe	Gly	Gln	Ala	Ala	Ala	Gly	Asp	Lys		
				85					90					95			
Pro	Ser	Pro	Phe	Gly	Gln	Ala	Ala	Ala	Gly	Asp	Lys	Pro	Pro	Pro	Phe		
			100					105					110				
Gly	Gln	Ala	Ala	Ala	Gly	Asp	Lys	Pro	Ser	Leu	Phe	Gly	Gln	Ala	Ala		
		115					120						125				
Ala	Gly	Asp	Lys	Pro	Ser	Pro	Phe	Gly	Gln	Ala	Ala	Ala	Gly	Asp	Lys		
	130						135					140					
Pro	Pro	Pro	Phe	Gly	Gln	Ala	Ala	Ala	Gly	Asp	Lys	Pro	Pro	Pro	Phe		
145					150					155						160	
Gly	Gln	Ala	Ala	Ala	Gly	Asp	Lys	Pro	Ser	Leu	Phe	Gly	Gln	Ala	Ala		
				165					170					175			
Ala	Gly	Asp	Lys	Pro	Ser	Pro	Phe	Gly	Gln	Gly	Thr	Ala	Phe	Asp	Ala		
			180					185					190				
Ser	Arg	Ser	Thr	Val	Phe	Ala	Asn	Ala	Pro	Gly	Val	Ala	Gln	Val	Met		
		195					200						205				
Glu	Gln	Glu	Arg	Arg	Gln	Leu	Leu	Glu	Lys	Asp	Pro	Arg	Arg	Asn	Ala		
	210					215					220						
Lys	Glu	Ile	Ala	Ala	Leu	Glu	Glu	Ser	Met	Asn	Ala	Arg	Ala	Gln	Glu		
225						230				235					240		
Leu	Ala	Arg	Glu	Lys	Lys	Leu	Ala	Asp	Arg	Ala	Phe	Leu	Asp	Gln	Lys		
				245					250					255			
Pro	Glu	Gly	Val	Pro	Leu	Arg	Glu	Leu	Pro	Leu	Asp	Asp	Asp	Ser	Asp		
			260					265					270				
Phe	Val	Ala	Met	Glu	Gln	Glu	Arg	Arg	Gln	Leu	Leu	Glu	Lys	Asp	Pro		
		275					280					285					
Arg	Arg	Asn	Ala	Lys	Glu	Ile	Ala	Ala	Leu	Glu	Glu	Ser	Met	Asn	Ala		
	290					295					300						
Arg	Ala	Gln	Glu	Leu	Ala	Arg	Glu	Lys	Lys	Leu	Ala	Asp	Arg	Ala	Phe		
305					310					315					320		
Leu	Asp	Gln	Lys	Pro	Glu	Gly	Val	Pro	Leu	Arg	Glu	Leu	Pro	Leu	Asp		
				325					330					335			
Asp	Asp	Ser	Asp	Phe	Val	Ala	Met	Glu	Gln	Glu	Arg	Arg	Gln	Leu	Leu		
			340					345					350				
Glu	Lys	Asp	Pro	Arg	Arg	Asn	Ala	Lys	Glu	Ile	Ala	Ala	Leu	Glu	Glu		
		355					360					365					

Ser Met Asn Ala Arg Ala Gln Glu Leu Ala Arg Glu Lys Lys Leu Ala
 370 375 380
 Asp Arg Ala Phe Leu Asp Gln Lys Pro Glu Gly Val Pro Leu Arg Glu
 385 390 395 400
 Leu Pro Leu Asp Asp Asp Ser Asp Phe Val Ala Met Glu Gln Glu Arg
 405 410 415
 Arg Gln Leu Leu Glu Lys Asp Pro Arg Arg Asn Ala Lys Glu Ile Ala
 420 425 430
 Ala Leu Glu Glu Ser Met Asn Ala Arg Ala Gln Glu Leu Ala Arg Glu
 435 440 445
 Lys Lys Leu Ala Asp Arg Ala Phe Leu Asp Gln Lys Pro Glu Gly Val
 450 455 460
 Pro Leu Arg Glu Leu Pro Leu Asp Asp Asp Ser Asp Phe Val Ala Met
 465 470 475 480
 Glu Gln Glu Arg Arg Gln Leu Leu Glu Lys Asp Pro Arg Arg Asn Ala
 485 490 495
 Lys Glu Ile Ala Ala Leu Glu Glu Ser Met Asn Ala Arg Ala Gln Glu
 500 505 510
 Leu Ala Arg Glu Lys Lys Leu Ala Asp Arg Ala Phe Leu Asp Gln Lys
 515 520 525
 Pro Glu Gly Val Pro Leu Arg Glu Leu Pro Leu Asp Asp Asp Ser Asp
 530 535 540
 Phe Val Ala Met Glu Gln Glu Arg Arg Gln Leu Leu Glu Lys Asp Pro
 545 550 555 560
 Arg Arg Asn Ala Lys Glu Ile Ala Ala Leu Glu Glu Ser Met Asn Ala
 565 570 575
 Arg Ala Gln Glu Leu Ala Arg Glu Lys Lys Leu Ala Asp Arg Ala Phe
 580 585 590
 Leu Asp Gln Lys Pro Glu Gly Val Pro Leu Arg Glu Leu Pro Leu Asp
 595 600 605
 Asp Asp Ser Asp Phe Val Ala
 610 615

<210> 43
 <211> 858
 <212> DNA
 <213> Trypanosoma cruzi

<220>
 <221> CDS
 <222> (1) .. (858)

<400> 43

gat cca acg tat cgt ttt gca aac cac gcg ttc acg ctg gtg gcg tcg	48
Asp Pro Thr Tyr Arg Phe Ala Asn His Ala Phe Thr Leu Val Ala Ser	
1 5 10 15	
gtg acg att cac gag gtt ccg agc gtc gcg agt cct ttg ctg ggt gcg	96
Val Thr Ile His Glu Val Pro Ser Val Ala Ser Pro Leu Leu Gly Ala	
20 25 30	
agc ctg gac tct tct ggt ggc aaa aaa ctc ctg ggg ctc tcg tac gac	144
Ser Leu Asp Ser Ser Gly Gly Lys Lys Leu Leu Gly Leu Ser Tyr Asp	
35 40 45	
gag aag cac cag tgg cag cca ata tac gga tca acg ccg gtg acg ccg	192
Glu Lys His Gln Trp Gln Pro Ile Tyr Gly Ser Thr Pro Val Thr Pro	
50 55 60	
acc gga tcg tgg gag atg ggt aag agg tac cac gtg gtt ctt acg atg	240
Thr Gly Ser Trp Glu Met Gly Lys Arg Tyr His Val Val Leu Thr Met	
65 70 75 80	
gcg aat aaa att ggc tcc gtg tac att gat gga gaa cct ctg gag ggt	288
Ala Asn Lys Ile Gly Ser Val Tyr Ile Asp Gly Glu Pro Leu Glu Gly	
85 90 95	
tca ggg cag acc gtt gtg cca gac gag agg acg cct gac atc tcc cac	336
Ser Gly Gln Thr Val Val Pro Asp Glu Arg Thr Pro Asp Ile Ser His	
100 105 110	
ttc tac gtt ggc ggg tat gga agg agt gat atg cca acc ata agc cac	384
Phe Tyr Val Gly Gly Tyr Gly Arg Ser Asp Met Pro Thr Ile Ser His	
115 120 125	
gtg acg gtg aat aat gtt ctt ctt tac aac cgt cag ctg aat gcc gag	432
Val Thr Val Asn Asn Val Leu Leu Tyr Asn Arg Gln Leu Asn Ala Glu	
130 135 140	
gag atc agg acc ttg ttc ttg agc cag gac ctg att ggc acg gaa gca	480
Glu Ile Arg Thr Leu Phe Leu Ser Gln Asp Leu Ile Gly Thr Glu Ala	
145 150 155 160	
cac atg ggc agc agc agc ggc agc agt gcc cac ggt acg ccc tcg att	528
His Met Gly Ser Ser Ser Gly Ser Ser Ala His Gly Thr Pro Ser Ile	
165 170 175	
ccc gtt gac agc agt gcc cac ggt aca ccc tcg act ccc gtt gac agc	576
Pro Val Asp Ser Ser Ala His Gly Thr Pro Ser Thr Pro Val Asp Ser	
180 185 190	
agt gcc cac ggt acg ccc tcg act ccc gtt gac agc agt gcc cac ggt	624
Ser Ala His Gly Thr Pro Ser Thr Pro Val Asp Ser Ser Ala His Gly	
195 200 205	
aca ccc tcg act ccc gtt gac agc agt gcc cac ggt aca ccc tcg act	672
Thr Pro Ser Thr Pro Val Asp Ser Ser Ala His Gly Thr Pro Ser Thr	
210 215 220	

ccc gtt gac agc agt gcc cac ggt aag ccc tcg act ccc gct gac agc 720
 Pro Val Asp Ser Ser Ala His Gly Lys Pro Ser Thr Pro Ala Asp Ser
 225 230 235 240

agt gcc cac agt acg ccc tcg act ccc gct gac agc agt gcc cac agt 768
 Ser Ala His Ser Thr Pro Ser Thr Pro Ala Asp Ser Ser Ala His Ser
 245 250 255

acg ccc tca att ccc gct gac agc agt gcc cac agt acg ccc tca gct 816
 Thr Pro Ser Ile Pro Ala Asp Ser Ser Ala His Ser Thr Pro Ser Ala
 260 265 270

ccc gct gac aac ggc gcc aat ggt acg gtt ttg att ttg tcg 858
 Pro Ala Asp Asn Gly Ala Asn Gly Thr Val Leu Ile Leu Ser
 275 280 285

<210> 44

<211> 286

<212> PRT

<213> Trypanosoma cruzi

<400> 44

Asp Pro Thr Tyr Arg Phe Ala Asn His Ala Phe Thr Leu Val Ala Ser
 1 5 10 15

Val Thr Ile His Glu Val Pro Ser Val Ala Ser Pro Leu Leu Gly Ala
 20 25 30

Ser Leu Asp Ser Ser Gly Gly Lys Lys Leu Leu Gly Leu Ser Tyr Asp
 35 40 45

Glu Lys His Gln Trp Gln Pro Ile Tyr Gly Ser Thr Pro Val Thr Pro
 50 55 60

Thr Gly Ser Trp Glu Met Gly Lys Arg Tyr His Val Val Leu Thr Met
 65 70 75 80

Ala Asn Lys Ile Gly Ser Val Tyr Ile Asp Gly Glu Pro Leu Glu Gly
 85 90 95

Ser Gly Gln Thr Val Val Pro Asp Glu Arg Thr Pro Asp Ile Ser His
 100 105 110

Phe Tyr Val Gly Gly Tyr Gly Arg Ser Asp Met Pro Thr Ile Ser His
 115 120 125

Val Thr Val Asn Asn Val Leu Leu Tyr Asn Arg Gln Leu Asn Ala Glu
 130 135 140

Glu Ile Arg Thr Leu Phe Leu Ser Gln Asp Leu Ile Gly Thr Glu Ala
 145 150 155 160

His Met Gly Ser Ser Ser Gly Ser Ser Ala His Gly Thr Pro Ser Ile
 165 170 175

Pro Val Asp Ser Ser Ala His Gly Thr Pro Ser Thr Pro Val Asp Ser
 180 185 190

Ser Ala His Gly Thr Pro Ser Thr Pro Val Asp Ser Ser Ala His Gly
 195 200 205

Thr Pro Ser Thr Pro Val Asp Ser Ser Ala His Gly Thr Pro Ser Thr
 210 215 220

Pro Val Asp Ser Ser Ala His Gly Lys Pro Ser Thr Pro Ala Asp Ser
 225 230 235 240

Ser Ala His Ser Thr Pro Ser Thr Pro Ala Asp Ser Ser Ala His Ser
 245 250 255

Thr Pro Ser Ile Pro Ala Asp Ser Ser Ala His Ser Thr Pro Ser Ala
 260 265 270

Pro Ala Asp Asn Gly Ala Asn Gly Thr Val Leu Ile Leu Ser
 275 280 285

<210> 45
 <211> 701
 <212> DNA
 <213> Trypanosoma cruzi

<220>
 <221> CDS
 <222> (1)..(699)

<400> 45
 act cat gac gcg tac agg ccc gtt gat ccc tcg gcg tac aag cgc gcc 48
 Thr His Asp Ala Tyr Arg Pro Val Asp Pro Ser Ala Tyr Lys Arg Ala
 1 5 10 15

ttg ccg cag gaa gag caa gag gat gtg ggg ccg cgc cac gtt gat ccc 96
 Leu Pro Gln Glu Glu Gln Glu Asp Val Gly Pro Arg His Val Asp Pro
 20 25 30

gac cac ttc cgc tcg acc tcg acg act cat gac gcg tac agg ccc gtt 144
 Asp His Phe Arg Ser Thr Ser Thr Thr His Asp Ala Tyr Arg Pro Val
 35 40 45

gat ccc tcg gcg tac aag cgc gcc ttg ccg cag gaa gag caa gag gat 192
 Asp Pro Ser Ala Tyr Lys Arg Ala Leu Pro Gln Glu Glu Gln Glu Asp
 50 55 60

gtg ggg ccg cgc cac gtt gat ccc gac cac ttc cgc tcg acg act cat 240
 Val Gly Pro Arg His Val Asp Pro Asp His Phe Arg Ser Thr Thr His
 65 70 75 80

gac gcg tac agg ccc gtt gat ccc tcg gcg tac aag cgc gcc ttg ccg 288
 Asp Ala Tyr Arg Pro Val Asp Pro Ser Ala Tyr Lys Arg Ala Leu Pro
 85 90 95

cag gaa gag caa gag gat gtg ggg ccg cgc cac gtt gat ccc gac cac 336
 Gln Glu Glu Gln Glu Asp Val Gly Pro Arg His Val Asp Pro Asp His
 100 105 110

ttc cgc tcg acc tcg acg act cat gac gcg tac agg ccc gtt gat ccc	384
Phe Arg Ser Thr Ser Thr Thr His Asp Ala Tyr Arg Pro Val Asp Pro	
115 120 125	
tcg gcg tac aag cgc gcc ttg ccg cag gaa gag caa gag gat gtg ggg	432
Ser Ala Tyr Lys Arg Ala Leu Pro Gln Glu Glu Gln Glu Asp Val Gly	
130 135 140	
ccg cgc cac gtt gat ccc gac cac ttc cgc tcg acc tcg acg act cat	480
Pro Arg His Val Asp Pro Asp His Phe Arg Ser Thr Ser Thr Thr His	
145 150 155 160	
gac gcg tac agg ccc gtt gat ccc tcg gcg tac aag cgc gcc ttg ccg	528
Asp Ala Tyr Arg Pro Val Asp Pro Ser Ala Tyr Lys Arg Ala Leu Pro	
165 170 175	
cag gaa gag caa gag gat gtg ggg ccg cgc cac gtt gat ccc gac cac	576
Gln Glu Glu Gln Glu Asp Val Gly Pro Arg His Val Asp Pro Asp His	
180 185 190	
ttc cgc tcg acg act cat gac gcg tac agg ccc gtt gat ccc tcg gcg	624
Phe Arg Ser Thr Thr His Asp Ala Tyr Arg Pro Val Asp Pro Ser Ala	
195 200 205	
tac aag cgc gcc ttg ccg cag gaa gag caa gag gat gtg ggg ccg cgc	672
Tyr Lys Arg Ala Leu Pro Gln Glu Glu Gln Glu Asp Val Gly Pro Arg	
210 215 220	
cac gtt gat ccc gac cac ttc cgc tcg ac	701
His Val Asp Pro Asp His Phe Arg Ser	
225 230	

<210> 46

<211> 233

<212> PRT

<213> Trypanosoma cruzi

<400> 46

Thr His Asp Ala Tyr Arg Pro Val Asp Pro Ser Ala Tyr Lys Arg Ala	
1 5 10 15	
Leu Pro Gln Glu Glu Gln Glu Asp Val Gly Pro Arg His Val Asp Pro	
20 25 30	
Asp His Phe Arg Ser Thr Ser Thr Thr His Asp Ala Tyr Arg Pro Val	
35 40 45	
Asp Pro Ser Ala Tyr Lys Arg Ala Leu Pro Gln Glu Glu Gln Glu Asp	
50 55 60	
Val Gly Pro Arg His Val Asp Pro Asp His Phe Arg Ser Thr Thr His	
65 70 75 80	
Asp Ala Tyr Arg Pro Val Asp Pro Ser Ala Tyr Lys Arg Ala Leu Pro	
85 90 95	

Gln Glu Glu Gln Glu Asp Val Gly Pro Arg His Val Asp Pro Asp His
 100 105 110
 Phe Arg Ser Thr Ser Thr Thr His Asp Ala Tyr Arg Pro Val Asp Pro
 115 120 125
 Ser Ala Tyr Lys Arg Ala Leu Pro Gln Glu Glu Gln Glu Asp Val Gly
 130 135 140
 Pro Arg His Val Asp Pro Asp His Phe Arg Ser Thr Ser Thr Thr His
 145 150 155 160
 Asp Ala Tyr Arg Pro Val Asp Pro Ser Ala Tyr Lys Arg Ala Leu Pro
 165 170 175
 Gln Glu Glu Gln Glu Asp Val Gly Pro Arg His Val Asp Pro Asp His
 180 185 190
 Phe Arg Ser Thr Thr His Asp Ala Tyr Arg Pro Val Asp Pro Ser Ala
 195 200 205
 Tyr Lys Arg Ala Leu Pro Gln Glu Glu Gln Glu Asp Val Gly Pro Arg
 210 215 220
 His Val Asp Pro Asp His Phe Arg Ser
 225 230

<210> 47
 <211> 1557
 <212> DNA
 <213> Trypanosoma cruzi

<220>
 <221> CDS
 <222> (1)..(1557)

<400> 47
 gat cca acg tat cgt ttt gca aac cac gcg ttc acg ctg gtg gcg tcg 48
 Asp Pro Thr Tyr Arg Phe Ala Asn His Ala Phe Thr Leu Val Ala Ser
 1 5 10 15
 gtg acg att cac gag gtt ccg agc gtc gcg agt cct ttg ctg ggt gcg 96
 Val Thr Ile His Glu Val Pro Ser Val Ala Ser Pro Leu Leu Gly Ala
 20 25 30
 agc ctg gac tct tct ggt ggc aaa aaa ctc ctg ggg ctc tcg tac gac 144
 Ser Leu Asp Ser Ser Gly Gly Lys Lys Leu Leu Gly Leu Ser Tyr Asp
 35 40 45
 gag aag cac cag tgg cag cca ata tac gga tca acg ccg gtg acg ccg 192
 Glu Lys His Gln Trp Gln Pro Ile Tyr Gly Ser Thr Pro Val Thr Pro
 50 55 60
 acc gga tcg tgg gag atg ggt aag agg tac cac gtg gtt ctt acg atg 240
 Thr Gly Ser Trp Glu Met Gly Lys Arg Tyr His Val Val Leu Thr Met
 65 70 75 80

gcg aat aaa att ggc tcc gtg tac att gat gga gaa cct ctg gag ggt	288
Ala Asn Lys Ile Gly Ser Val Tyr Ile Asp Gly Glu Pro Leu Glu Gly	
85 90 95	
tca ggg cag acc gtt gtg cca gac gag agg acg cct gac atc tcc cac	336
Ser Gly Gln Thr Val Val Pro Asp Glu Arg Thr Pro Asp Ile Ser His	
100 105 110	
ttc tac gtt ggc ggg tat gga agg agt gat atg cca acc ata agc cac	384
Phe Tyr Val Gly Gly Tyr Gly Arg Ser Asp Met Pro Thr Ile Ser His	
115 120 125	
gtg acg gtg aat aat gtt ctt ctt tac aac cgt cag ctg aat gcc gag	432
Val Thr Val Asn Asn Val Leu Leu Tyr Asn Arg Gln Leu Asn Ala Glu	
130 135 140	
gag atc agg acc ttg ttc ttg agc cag gac ctg att ggc acg gaa gca	480
Glu Ile Arg Thr Leu Phe Leu Ser Gln Asp Leu Ile Gly Thr Glu Ala	
145 150 155 160	
cac atg ggc agc agc agc ggc agc agt gcc cac ggt acg ccc tcg att	528
His Met Gly Ser Ser Ser Gly Ser Ser Ala His Gly Thr Pro Ser Ile	
165 170 175	
ccc gtt gac agc agt gcc cac ggt aca ccc tcg act ccc gtt gac agc	576
Pro Val Asp Ser Ser Ala His Gly Thr Pro Ser Thr Pro Val Asp Ser	
180 185 190	
agt gcc cac ggt acg ccc tcg act ccc gtt gac agc agt gcc cac ggt	624
Ser Ala His Gly Thr Pro Ser Thr Pro Val Asp Ser Ser Ala His Gly	
195 200 205	
aca ccc tcg act ccc gtt gac agc agt gcc cac ggt aca ccc tcg act	672
Thr Pro Ser Thr Pro Val Asp Ser Ser Ala His Gly Thr Pro Ser Thr	
210 215 220	
ccc gtt gac agc agt gcc cac ggt aag ccc tcg act ccc gct gac agc	720
Pro Val Asp Ser Ser Ala His Gly Lys Pro Ser Thr Pro Ala Asp Ser	
225 230 235 240	
agt gcc cac agt acg ccc tcg act ccc gct gac agc agt gcc cac agt	768
Ser Ala His Ser Thr Pro Ser Thr Pro Ala Asp Ser Ser Ala His Ser	
245 250 255	
acg ccc tca att ccc gct gac agc agt gcc cac agt acg ccc tca gct	816
Thr Pro Ser Ile Pro Ala Asp Ser Ser Ala His Ser Thr Pro Ser Ala	
260 265 270	
ccc gct gac aac ggc gcc aat ggt acg gtt ttg att ttg tcg act cat	864
Pro Ala Asp Asn Gly Ala Asn Gly Thr Val Leu Ile Leu Ser Thr His	
275 280 285	
gac gcg tac agg ccc gtt gat ccc tcg gcg tac aag cgc gcc ttg ccg	912
Asp Ala Tyr Arg Pro Val Asp Pro Ser Ala Tyr Lys Arg Ala Leu Pro	
290 295 300	

cag gaa gag caa gag gat gtg ggg ccg cgc cac gtt gat ccc gac cac	960
Gln Glu Glu Gln Glu Asp Val Gly Pro Arg His Val Asp Pro Asp His	
305 310 315 320	
ttc cgc tcg acc tcg acg act cat gac gcg tac agg ccc gtt gat ccc	1008
Phe Arg Ser Thr Ser Thr Thr His Asp Ala Tyr Arg Pro Val Asp Pro	
325 330 335	
tcg gcg tac aag cgc gcc ttg ccg cag gaa gag caa gag gat gtg ggg	1056
Ser Ala Tyr Lys Arg Ala Leu Pro Gln Glu Glu Gln Glu Asp Val Gly	
340 345 350	
ccg cgc cac gtt gat ccc gac cac ttc cgc tcg acg act cat gac gcg	1104
Pro Arg His Val Asp Pro Asp His Phe Arg Ser Thr Thr His Asp Ala	
355 360 365	
tac agg ccc gtt gat ccc tcg gcg tac aag cgc gcc ttg ccg cag gaa	1152
Tyr Arg Pro Val Asp Pro Ser Ala Tyr Lys Arg Ala Leu Pro Gln Glu	
370 375 380	
gag caa gag gat gtg ggg ccg cgc cac gtt gat ccc gac cac ttc cgc	1200
Glu Gln Glu Asp Val Gly Pro Arg His Val Asp Pro Asp His Phe Arg	
385 390 395 400	
tcg acc tcg acg act cat gac gcg tac agg ccc gtt gat ccc tcg gcg	1248
Ser Thr Ser Thr Thr His Asp Ala Tyr Arg Pro Val Asp Pro Ser Ala	
405 410 415	
tac aag cgc gcc ttg ccg cag gaa gag caa gag gat gtg ggg ccg cgc	1296
Tyr Lys Arg Ala Leu Pro Gln Glu Glu Gln Glu Asp Val Gly Pro Arg	
420 425 430	
cac gtt gat ccc gac cac ttc cgc tcg acc tcg acg act cat gac gcg	1344
His Val Asp Pro Asp His Phe Arg Ser Thr Ser Thr Thr His Asp Ala	
435 440 445	
tac agg ccc gtt gat ccc tcg gcg tac aag cgc gcc ttg ccg cag gaa	1392
Tyr Arg Pro Val Asp Pro Ser Ala Tyr Lys Arg Ala Leu Pro Gln Glu	
450 455 460	
gag caa gag gat gtg ggg ccg cgc cac gtt gat ccc gac cac ttc cgc	1440
Glu Gln Glu Asp Val Gly Pro Arg His Val Asp Pro Asp His Phe Arg	
465 470 475 480	
tcg acg act cat gac gcg tac agg ccc gtt gat ccc tcg gcg tac aag	1488
Ser Thr Thr His Asp Ala Tyr Arg Pro Val Asp Pro Ser Ala Tyr Lys	
485 490 495	
cgc gcc ttg ccg cag gaa gag caa gag gat gtg ggg ccg cgc cac gtt	1536
Arg Ala Leu Pro Gln Glu Glu Gln Glu Asp Val Gly Pro Arg His Val	
500 505 510	
gat ccc gac cac ttc cgc tcg	1557
Asp Pro Asp His Phe Arg Ser	
515	

<210> 48

<211> 519

<212> PRT

<213> Trypanosoma cruzi

<400> 48

```

Asp Pro Thr Tyr Arg Phe Ala Asn His Ala Phe Thr Leu Val Ala Ser
 1              5              10              15

Val Thr Ile His Glu Val Pro Ser Val Ala Ser Pro Leu Leu Gly Ala
      20              25              30

Ser Leu Asp Ser Ser Gly Gly Lys Lys Leu Leu Gly Leu Ser Tyr Asp
      35              40              45

Glu Lys His Gln Trp Gln Pro Ile Tyr Gly Ser Thr Pro Val Thr Pro
      50              55              60

Thr Gly Ser Trp Glu Met Gly Lys Arg Tyr His Val Val Leu Thr Met
      65              70              75              80

Ala Asn Lys Ile Gly Ser Val Tyr Ile Asp Gly Glu Pro Leu Glu Gly
      85              90              95

Ser Gly Gln Thr Val Val Pro Asp Glu Arg Thr Pro Asp Ile Ser His
      100             105             110

Phe Tyr Val Gly Gly Tyr Gly Arg Ser Asp Met Pro Thr Ile Ser His
      115             120             125

Val Thr Val Asn Asn Val Leu Leu Tyr Asn Arg Gln Leu Asn Ala Glu
      130             135             140

Glu Ile Arg Thr Leu Phe Leu Ser Gln Asp Leu Ile Gly Thr Glu Ala
      145             150             155             160

His Met Gly Ser Ser Ser Gly Ser Ser Ala His Gly Thr Pro Ser Ile
      165             170             175

Pro Val Asp Ser Ser Ala His Gly Thr Pro Ser Thr Pro Val Asp Ser
      180             185             190

Ser Ala His Gly Thr Pro Ser Thr Pro Val Asp Ser Ser Ala His Gly
      195             200             205

Thr Pro Ser Thr Pro Val Asp Ser Ser Ala His Gly Thr Pro Ser Thr
      210             215             220

Pro Val Asp Ser Ser Ala His Gly Lys Pro Ser Thr Pro Ala Asp Ser
      225             230             235             240

Ser Ala His Ser Thr Pro Ser Thr Pro Ala Asp Ser Ser Ala His Ser
      245             250             255

Thr Pro Ser Ile Pro Ala Asp Ser Ser Ala His Ser Thr Pro Ser Ala
      260             265             270

```

Pro Ala Asp Asn Gly Ala Asn Gly Thr Val Leu Ile Leu Ser Thr His
 275 280 285
 Asp Ala Tyr Arg Pro Val Asp Pro Ser Ala Tyr Lys Arg Ala Leu Pro
 290 295 300
 Gln Glu Glu Gln Glu Asp Val Gly Pro Arg His Val Asp Pro Asp His
 305 310 315 320
 Phe Arg Ser Thr Ser Thr Thr His Asp Ala Tyr Arg Pro Val Asp Pro
 325 330 335
 Ser Ala Tyr Lys Arg Ala Leu Pro Gln Glu Glu Gln Glu Asp Val Gly
 340 345 350
 Pro Arg His Val Asp Pro Asp His Phe Arg Ser Thr Thr His Asp Ala
 355 360 365
 Tyr Arg Pro Val Asp Pro Ser Ala Tyr Lys Arg Ala Leu Pro Gln Glu
 370 375 380
 Glu Gln Glu Asp Val Gly Pro Arg His Val Asp Pro Asp His Phe Arg
 385 390 395 400
 Ser Thr Ser Thr Thr His Asp Ala Tyr Arg Pro Val Asp Pro Ser Ala
 405 410 415
 Tyr Lys Arg Ala Leu Pro Gln Glu Glu Gln Glu Asp Val Gly Pro Arg
 420 425 430
 His Val Asp Pro Asp His Phe Arg Ser Thr Ser Thr Thr His Asp Ala
 435 440 445
 Tyr Arg Pro Val Asp Pro Ser Ala Tyr Lys Arg Ala Leu Pro Gln Glu
 450 455 460
 Glu Gln Glu Asp Val Gly Pro Arg His Val Asp Pro Asp His Phe Arg
 465 470 475 480
 Ser Thr Thr His Asp Ala Tyr Arg Pro Val Asp Pro Ser Ala Tyr Lys
 485 490 495
 Arg Ala Leu Pro Gln Glu Glu Gln Glu Asp Val Gly Pro Arg His Val
 500 505 510
 Asp Pro Asp His Phe Arg Ser
 515

<210> 49

<211> 1521

<212> DNA

<213> Trypanosoma cruzi

<220>

<221> CDS

<222> (1)..(1521)

<400> 49

atg gcc cga gct gtg gtg ctt gag gat gga gcg ctt tac gtg gcg gac	48
Met Ala Arg Ala Val Val Leu Glu Asp Gly Ala Leu Tyr Val Ala Asp	
1 5 10 15	
aat gcc aac aac ctc gtt cga gaa atc tcc aat ggc gtt gtc act tcg	96
Asn Ala Asn Asn Leu Val Arg Glu Ile Ser Asn Gly Val Val Thr Ser	
20 25 30	
ttt att acg gaa gga ctg ctg ggc cca tcg tac atc aaa ccg tac agc	144
Phe Ile Thr Glu Gly Leu Leu Gly Pro Ser Tyr Ile Lys Pro Tyr Ser	
35 40 45	
cgt aca aat ggc gct cat gac ttg ttt gtg tcg gac acg ggc aaa tca	192
Arg Thr Asn Gly Ala His Asp Leu Phe Val Ser Asp Thr Gly Lys Ser	
50 55 60	
cgc atc att ttt gcc cca cct cag aaa aaa acg ttc atc aca gtg ttt	240
Arg Ile Ile Phe Ala Pro Pro Gln Lys Lys Thr Phe Ile Thr Val Phe	
65 70 75 80	
ata aca gga ttc cag ccg gat gtt ctt caa att agc gag aag agt cgt	288
Ile Thr Gly Phe Gln Pro Asp Val Leu Gln Ile Ser Glu Lys Ser Arg	
85 90 95	
ttg atg ttt gcc atc tgc aat tcc acg aaa att ctt gcg att aat atg	336
Leu Met Phe Ala Ile Cys Asn Ser Thr Lys Ile Leu Ala Ile Asn Met	
100 105 110	
cag gga gcc aca acc ccg aag gag tac tgg caa gtt gga aat gcg gac	384
Gln Gly Ala Thr Thr Pro Lys Glu Tyr Trp Gln Val Gly Asn Ala Asp	
115 120 125	
tgc atg ggc tat cag agt tcc ctc atg ctc acg acc gag gag gat aaa	432
Cys Met Gly Tyr Gln Ser Ser Leu Met Leu Thr Thr Glu Glu Asp Lys	
130 135 140	
ctc ctc tac tac ggc ata tta aat gga acc cca tcc atc atg tct tta	480
Leu Leu Tyr Tyr Gly Ile Leu Asn Gly Thr Pro Ser Ile Met Ser Leu	
145 150 155 160	
ccc gcc acc aaa acg aag acg gaa gca ccc aga att tgc ccg gat gtg	528
Pro Ala Thr Lys Thr Lys Thr Glu Ala Pro Arg Ile Cys Pro Asp Val	
165 170 175	
ttg ttg cag tgg cca cat ggg ccc att gtt tcg ctt gtg aat att aac	576
Leu Leu Gln Trp Pro His Gly Pro Ile Val Ser Leu Val Asn Ile Asn	
180 185 190	
aaa cat gca ttt tac gtt gtt acc gcc tcc aat gta tac att gta cat	624
Lys His Ala Phe Tyr Val Val Thr Ala Ser Asn Val Tyr Ile Val His	
195 200 205	
gat ggc tcg tat cat ccg act gga tcc atg gcc cag ctc caa cag gca	672
Asp Gly Ser Tyr His Pro Thr Gly Ser Met Ala Gln Leu Gln Gln Ala	
210 215 220	

gaa aat aat atc act aat tcc aaa aaa gaa atg aca aag cta cga gaa	720
Glu Asn Asn Ile Thr Asn Ser Lys Lys Glu Met Thr Lys Leu Arg Glu	
225 230 235 240	
aaa gtg aaa aag gcc gag aaa gaa aaa ttg gac gcc att aac cgg gca	768
Lys Val Lys Lys Ala Glu Lys Glu Lys Leu Asp Ala Ile Asn Arg Ala	
245 250 255	
acc aag ctg gaa gag gaa cga aac caa gcg tac aaa gca gca cac aag	816
Thr Lys Leu Glu Glu Glu Arg Asn Gln Ala Tyr Lys Ala Ala His Lys	
260 265 270	
gca gag gag gaa aag gct aaa aca ttt caa cgc ctt ata aca ttt gag	864
Ala Glu Glu Glu Lys Ala Lys Thr Phe Gln Arg Leu Ile Thr Phe Glu	
275 280 285	
tcg gaa aat att aac tta aag aaa agg cca aat gac gca gtt tca aat	912
Ser Glu Asn Ile Asn Leu Lys Lys Arg Pro Asn Asp Ala Val Ser Asn	
290 295 300	
cgg gat aag aaa aaa aat tct gaa acc gca aaa act gac gaa gta gag	960
Arg Asp Lys Lys Lys Asn Ser Glu Thr Ala Lys Thr Asp Glu Val Glu	
305 310 315 320	
aaa cag agg gcg gct gag gct gcc aag gcc gtg gag acg gag aag cag	1008
Lys Gln Arg Ala Ala Glu Ala Ala Lys Ala Val Glu Thr Glu Lys Gln	
325 330 335	
agg gca gct gag gcc acg aag gtt gcc gaa gcg gag aag cgg aag gca	1056
Arg Ala Ala Glu Ala Thr Lys Val Ala Glu Ala Glu Lys Arg Lys Ala	
340 345 350	
gct gag gcc gcc aag gcc gtg gag acg gag aag cag agg gca gct gaa	1104
Ala Glu Ala Ala Lys Ala Val Glu Thr Glu Lys Gln Arg Ala Ala Glu	
355 360 365	
gcc acg aag gtt gcc gaa gcg gag aag cag aag gca gct gag gcc gcc	1152
Ala Thr Lys Val Ala Glu Ala Glu Lys Gln Lys Ala Ala Glu Ala Ala	
370 375 380	
aag gcc gtg gag acg gag aag cag agg gca gct gaa gcc acg aag gtt	1200
Lys Ala Val Glu Thr Glu Lys Gln Arg Ala Ala Glu Ala Thr Lys Val	
385 390 395 400	
gcc gaa gcg gag aag cag agg gca gct gaa gcc atg aag gtt gcc gaa	1248
Ala Glu Ala Glu Lys Gln Arg Ala Ala Glu Ala Met Lys Val Ala Glu	
405 410 415	
gcg gag aag cag aag gca gct gag gcc gcc aag gcc gtg gag acg gag	1296
Ala Glu Lys Gln Lys Ala Ala Glu Ala Ala Lys Ala Val Glu Thr Glu	
420 425 430	
aag cag agg gca gct gaa gcc acg aag gtt gcc gaa gcg gag aag cag	1344
Lys Gln Arg Ala Ala Glu Ala Thr Lys Val Ala Glu Ala Glu Lys Gln	
435 440 445	

aag gca gct gag gcc gcc aag gcc gtg gag acg gag aag cag agg gca 1392
 Lys Ala Ala Glu Ala Ala Lys Ala Val Glu Thr Glu Lys Gln Arg Ala
 450 455 460

gct gaa gcc acg aag gtt gcc gaa gcg gag aag cag aag gca gct gag 1440
 Ala Glu Ala Thr Lys Val Ala Glu Ala Glu Lys Gln Lys Ala Ala Glu
 465 470 475 480

gcc gcc aag gcc gtg gag acg gag aag cag agg gca gct gaa gcc acg 1488
 Ala Ala Lys Ala Val Glu Thr Glu Lys Gln Arg Ala Ala Glu Ala Thr
 485 490 495

aag gtt gcc gaa gcg gag aag gat atc gat ccc 1521
 Lys Val Ala Glu Ala Glu Lys Asp Ile Asp Pro
 500 505

<210> 50

<211> 507

<212> PRT

<213> Trypanosoma cruzi

<400> 50

Met Ala Arg Ala Val Val Leu Glu Asp Gly Ala Leu Tyr Val Ala Asp
 1 5 10 15

Asn Ala Asn Asn Leu Val Arg Glu Ile Ser Asn Gly Val Val Thr Ser
 20 25 30

Phe Ile Thr Glu Gly Leu Leu Gly Pro Ser Tyr Ile Lys Pro Tyr Ser
 35 40 45

Arg Thr Asn Gly Ala His Asp Leu Phe Val Ser Asp Thr Gly Lys Ser
 50 55 60

Arg Ile Ile Phe Ala Pro Pro Gln Lys Lys Thr Phe Ile Thr Val Phe
 65 70 75 80

Ile Thr Gly Phe Gln Pro Asp Val Leu Gln Ile Ser Glu Lys Ser Arg
 85 90 95

Leu Met Phe Ala Ile Cys Asn Ser Thr Lys Ile Leu Ala Ile Asn Met
 100 105 110

Gln Gly Ala Thr Thr Pro Lys Glu Tyr Trp Gln Val Gly Asn Ala Asp
 115 120 125

Cys Met Gly Tyr Gln Ser Ser Leu Met Leu Thr Thr Glu Glu Asp Lys
 130 135 140

Leu Leu Tyr Tyr Gly Ile Leu Asn Gly Thr Pro Ser Ile Met Ser Leu
 145 150 155 160

Pro Ala Thr Lys Thr Lys Thr Glu Ala Pro Arg Ile Cys Pro Asp Val
 165 170 175

Leu Leu Gln Trp Pro His Gly Pro Ile Val Ser Leu Val Asn Ile Asn
 180 185 190

Lys	His	Ala	Phe	Tyr	Val	Val	Thr	Ala	Ser	Asn	Val	Tyr	Ile	Val	His	195	200	205	
Asp	Gly	Ser	Tyr	His	Pro	Thr	Gly	Ser	Met	Ala	Gln	Leu	Gln	Gln	Ala	210	215	220	
Glu	Asn	Asn	Ile	Thr	Asn	Ser	Lys	Lys	Glu	Met	Thr	Lys	Leu	Arg	Glu	225	230	235	240
Lys	Val	Lys	Lys	Ala	Glu	Lys	Glu	Lys	Leu	Asp	Ala	Ile	Asn	Arg	Ala	245	250	255	
Thr	Lys	Leu	Glu	Glu	Glu	Arg	Asn	Gln	Ala	Tyr	Lys	Ala	Ala	His	Lys	260	265	270	
Ala	Glu	Glu	Glu	Lys	Ala	Lys	Thr	Phe	Gln	Arg	Leu	Ile	Thr	Phe	Glu	275	280	285	
Ser	Glu	Asn	Ile	Asn	Leu	Lys	Lys	Arg	Pro	Asn	Asp	Ala	Val	Ser	Asn	290	295	300	
Arg	Asp	Lys	Lys	Lys	Asn	Ser	Glu	Thr	Ala	Lys	Thr	Asp	Glu	Val	Glu	305	310	315	320
Lys	Gln	Arg	Ala	Ala	Glu	Ala	Ala	Lys	Ala	Val	Glu	Thr	Glu	Lys	Gln	325	330	335	
Arg	Ala	Ala	Glu	Ala	Thr	Lys	Val	Ala	Glu	Ala	Glu	Lys	Arg	Lys	Ala	340	345	350	
Ala	Glu	Ala	Ala	Lys	Ala	Val	Glu	Thr	Glu	Lys	Gln	Arg	Ala	Ala	Glu	355	360	365	
Ala	Thr	Lys	Val	Ala	Glu	Ala	Glu	Lys	Gln	Lys	Ala	Ala	Glu	Ala	Ala	370	375	380	
Lys	Ala	Val	Glu	Thr	Glu	Lys	Gln	Arg	Ala	Ala	Glu	Ala	Thr	Lys	Val	385	390	395	400
Ala	Glu	Ala	Glu	Lys	Gln	Arg	Ala	Ala	Glu	Ala	Met	Lys	Val	Ala	Glu	405	410	415	
Ala	Glu	Lys	Gln	Lys	Ala	Ala	Glu	Ala	Ala	Lys	Ala	Val	Glu	Thr	Glu	420	425	430	
Lys	Gln	Arg	Ala	Ala	Glu	Ala	Thr	Lys	Val	Ala	Glu	Ala	Glu	Lys	Gln	435	440	445	
Lys	Ala	Ala	Glu	Ala	Ala	Lys	Ala	Val	Glu	Thr	Glu	Lys	Gln	Arg	Ala	450	455	460	
Ala	Glu	Ala	Thr	Lys	Val	Ala	Glu	Ala	Glu	Lys	Gln	Lys	Ala	Ala	Glu	465	470	475	480
Ala	Ala	Lys	Ala	Val	Glu	Thr	Glu	Lys	Gln	Arg	Ala	Ala	Glu	Ala	Thr	485	490	495	

Lys Val Ala Glu Ala Glu Lys Asp Ile Asp Pro
 500 505

<210> 51
 <211> 34
 <212> PRT
 <213> Trypanosoma cruzi

<400> 51
 Ser Thr Asp Lys Leu Lys Leu Asn Gln Gln Asn Lys Pro His Ile Ala
 1 5 10 15
 Asn Asn Lys Gln Lys Thr Thr Leu Glu Lys Thr Gln Thr Glu Gln Lys
 20 25 30
 Thr Ala

<210> 52
 <211> 12
 <212> PRT
 <213> Trypanosoma cruzi

<400> 52
 Pro Phe Gly Gln Ala Ala Ala Gly Asp Lys Pro Ser
 1 5 10

<210> 53
 <211> 21
 <212> PRT
 <213> Trypanosoma cruzi

<400> 53
 Gly Thr Ala Phe Asp Ala Ser Arg Ser Thr Val Phe Ala Asn Ala Pro
 1 5 10 15
 Gly Val Ala Gln Val
 20

<210> 54
 <211> 68
 <212> PRT
 <213> Trypanosoma cruzi

<400> 54
 Met Glu Gln Glu Arg Arg Gln Leu Leu Glu Lys Asp Pro Arg Arg Asn
 1 5 10 15
 Ala Lys Glu Ile Ala Ala Leu Glu Glu Ser Met Asn Ala Arg Ala Gln
 20 25 30
 Glu Leu Ala Arg Glu Lys Lys Leu Ala Asp Arg Ala Phe Leu Asp Gln
 35 40 45

Lys Pro Glu Gly Val Pro Leu Arg Glu Leu Pro Leu Asp Asp Asp Ser
 50 55 60

Asp Phe Val Ala
 65

<210> 55
 <211> 85
 <212> PRT
 <213> Trypanosoma cruzi

<400> 55
 Met Ala Gln Leu Gln Gln Ala Glu Asn Asn Ile Thr Asn Ser Lys Lys
 1 5 10 15
 Glu Met Thr Lys Leu Arg Glu Lys Val Lys Lys Ala Glu Lys Glu Lys
 20 25 30
 Leu Asp Ala Ile Asn Arg Ala Thr Lys Leu Glu Glu Glu Arg Asn Gln
 35 40 45
 Ala Tyr Lys Ala Ala His Lys Ala Glu Glu Glu Lys Ala Lys Thr Phe
 50 55 60
 Gln Arg Leu Ile Thr Phe Glu Ser Glu Asn Ile Asn Leu Lys Lys Arg
 65 70 75 80
 Pro Asn Asp Ala Val
 85

<210> 56
 <211> 14
 <212> PRT
 <213> Trypanosoma cruzi

<400> 56
 Gln Arg Ala Ala Glu Ala Ala Lys Ala Val Glu Thr Glu Lys
 1 5 10

<210> 57
 <211> 214
 <212> PRT
 <213> Trypanosoma cruzi

<400> 57
 Asp Ile Asp Pro Met Gly Ala Cys Gly Ser Lys Asp Ser Thr Ser Asp
 1 5 10 15
 Lys Gly Leu Ala Ser Asp Lys Asp Gly Lys Asn Ala Lys Asp Arg Lys
 20 25 30
 Glu Ala Trp Glu Arg Ile Arg Gln Ala Ile Pro Arg Glu Lys Thr Ala
 35 40 45

[illegible]